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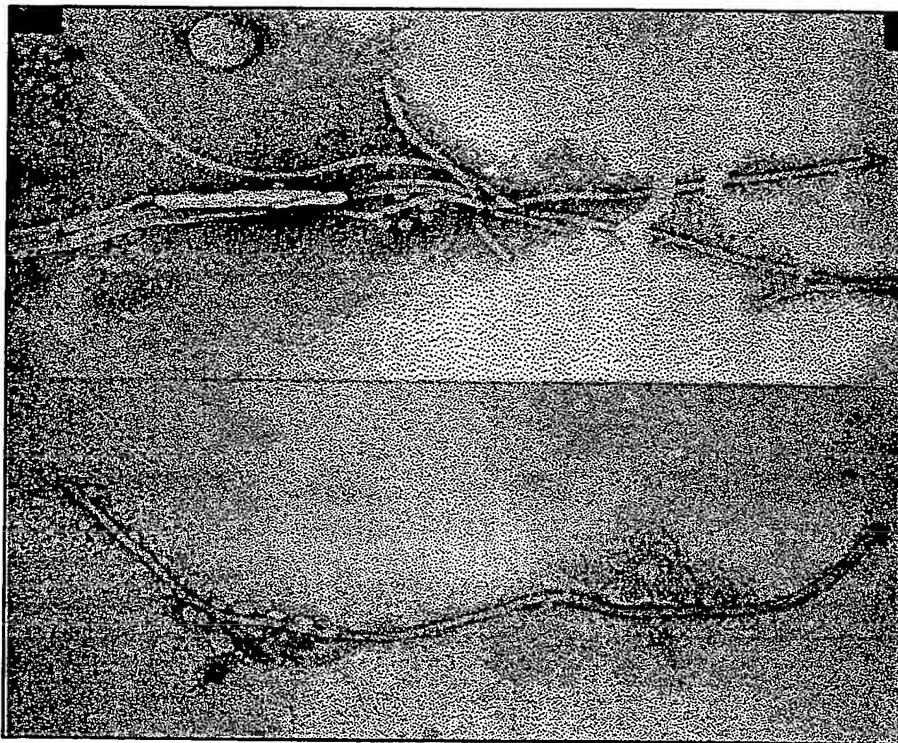


FIG. 1

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TGTGGACAGCAATCTTCCAAAGAAAGACAGGGATGACATCATGGAAGCGAGTCGACGACT
1 ----- (93-110) -----+-----+-----+-----+-----+-----+ 60
ACACCTGTCGTTAGAAGGTTTCTTTCTGTCCCTACTGTAGTACCTTCGCTCAGCTGCTGA
V D S N L P K K D R D D I M E A S R R L -

ATCGCCATCGGACGCCGCCTTTTGCAGAGCAGTGTCCGGTTCAGGTAGGGAAGTATGTGGA
61 -----+-----+-----+-----+-----+-----+ 120
TAGCGGTAGCCTGCGGCGGAAAACGTCTCGTCACAGCCAAGTCCATCCCTTCATACACCT
S P S D A A F C R A V S V Q V G K Y V D -

CGTAACGCAGAATTTAGAAAGTACGATCGTGCCGTTAAGAGTTATGGAAATAAGAAAAG
121 -----+----- (93-25) -----+-----+-----+-----+ 180
GCATTGCGTCTTAAATCTTTTCATGCTAGCACGGCAATTCTCAATACCTTTATTTCTTTTC
V T Q N L E S T I V P L R V M E I K K R -

ACGAGGATCAGCACATGTTAGTTTACCGAAGGTGGTATCCGCTTACGTAGATTTTTTATAC
181 -----+-----+-----+-----+-----+-----+ 240
TGCTCCTAGTTCGTGTACAATCAAATGGCTTCCACCATAGGCGAATGCATCTAAAAATATG
R G S A H V S L P K V V S A Y V D F Y T -

GAACTTGCAGGAATTGCTGTCCGATGAAGTAACTAGGGCCAGAACCGATACAGTTTTCGGC
241 -----+-----+-----+-----+-----+-----+ 300
CTTGAACGTCCTTAACGACAGCCTACTTCATTGATCCCGGTCTTGGCTATGTCAAAGCCG
N L Q E L L S D E V T R A R T D T V S A -

ATACGCTACCGACTCTATGGCTTTCTTAGTTAAGATGTTACCCCTGACTGCTCGTGAGCA
301 -----+-----+-----+-----+----- (93-40) -----+ 360
TATGCGATGGCTGAGATACCGAAAGAATCAATTCTACAATGGGGACTGACGAGCACTCGT
Y A T D S M A F L V K M L P L T A R E Q -

GTGGTTAAAAGACGTGCTAGGATATCTGCTAGTACGGAGACGACCAGCAAATTTTTCTTA
361 -----+-----+-----+-----+-----+-----+ 420
CACCAATTTTTCTGCACGATCCTATAGACGATCATGCCTCTGCTGGTCGTTTAAAAGGAT
W L K D V L G Y L L V R R R P A N F S Y -

CGACGTAAGAGTAGCTTGGGTATATGACGTGATCGCTACGCTCAAGCTGGTCATAAGATT
421 -----+-----+-----+-----+-----+-----+ 480
GCTGCATTCTCATCGAACCCATATACTGCACTAGCGATGCGAGTTCGACCAGTATTCTAA
D V R V A W V Y D V I A T L K L V I R L -

GTTTTTCAACAAGGACACACCCGGGGGTATTAAAGACTTAAACCGTGTGTGCCTATAGA
481 -----+-----+-----+-----+-----+-----+ 540
CAAAAAGTTGTTCTGTGTGGGCCCCCATAATTTCTGAATTTTGGCACACACGGATATCT
F F N K D T P G G I K D L K P C V P I E -

GTCATTGACCCCTTTCACGAGCTTTTCGTCCTATTTCTCTAGGTTAAGTTACGAGATGAC
541 -----+-----+-----+-----+-----+-----+ 600
CAGTAAGCTGGGGAAAGTGCTCGAAAGCAGGATAAAGAGATCCAATTCAATGCTCTACTG
S F D P F H E L S S Y F S R L S Y E M T -

GACAGGTAAAGGGGGAAAGATATGCCCCGAGATCGCCGAGAAGTTGGT
601 -----+-----+-----+-----+----- (92-98) ----- 648
CTGTCCATTTCCCCCTTTCTATACGGGCCTCTAGCGGCTCTTCAACCA
T G K G G K I C P E I A E K L -

FIG. 2

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BYV_p64 115_VGCKFNIQSVTEFVKKINGNVAEPSLVEHCWSLSNSCGELINPKDTKRFV
CTV_p61 108_VGCRFTLNDVESYLMRGEDEFADLAAVEHSWCLSNSCSRLLSSTEIDANK
LIYV_P59 131_EGCSFTEQQVVEKYPQVDSLVAKIL.....YRVCNSLKGKLLDLKDFENKN
GLRaV3_p55 114_VDSNLPKKDRDDIME..ASRRLSPSDAAFCRAVSVQVGKYVDVTQNLEST

CONSENSUS vgc-f----v-e-----a-----w--sns-g-l----d-----

BYV_p64 SLIFKGKDLAESTDEAIVS..SSYLDYLSHCLNLYETCNLSSNSGKKSLY
CTV_p61 TLVF.TKNFDSNISG..VT..TKLETYLSYCISLYKKHCM.KDDDYFNLI
LIYV_P59 ISGFEINTAQDSPTVADDN..ES.NDFFRECVDNQRYYSLSGSKLGKAK
GLRaV3_p55 IVPLRVMEIKKRRGSAHVSLPKVVSAYVDFYTNLQELLSDEVTRARTDTV

CONSENSUS ---f-----a-v-----yl--c-nl-----

BYV_p64 DEFLKHVIDYL...ENS DLEYRSPSDNPLVAGILYDMCFEYNTLKSTYLK
CTV_p61 LPMFNCLMKVL...ASLGLFYEKHADNPLLTGMLIEFCLENKVVYYSTFKV
LIYV_P59 LEANAYIFKILLKSASGEFDIDRLSRNPLAISKFMNLYTNHVTDSETFKS
GLRaV3_p55 SAYATDSMAFLVKMLPLT.....AREQWLKDVLGYLLVRRRPPANFSYDV

CONSENSUS -----L-----l-----npl----l--lc-----t---

BYV_p64 NIESFDCFLSLYLPLLSEVFSMNWERPAPDVRLLFELDAAELLLKVPTIN
CTV_p61 NLDNVRLFKSKVLPVLTVDISEPDDPVDERVLIPFDPTDFVLDLPKLN
LIYV_P59 KFEALKSIKTPFASFIIKKAFGIR.....LNFEDSKIFYALPKER
GLRaV3_p55 RVAWVYDVIATLKLVLIRLFFNKDTPGGIKDLKPCVPIESFDPFHELS...

CONSENSUS --e-----i---f-----d-----f---d-f--lp---

BYV_p64 MHDST...FLYKNKLRYLESYFEDDSNELIKVKVDSLL
CTV_p61 IHDTM...VVVGNIQIRQLEYVVESDALDDLSQHVDLRL
LIYV_P59 QSDVLSDDMMVESIVRDAASFTTVSDNNYLPERVDRFV
GLRaV3_p55SYFSRLSYEMTTGKGKICPEIAEKL

CONSENSUS --d-----r-l-----vd--l

FIG. 3

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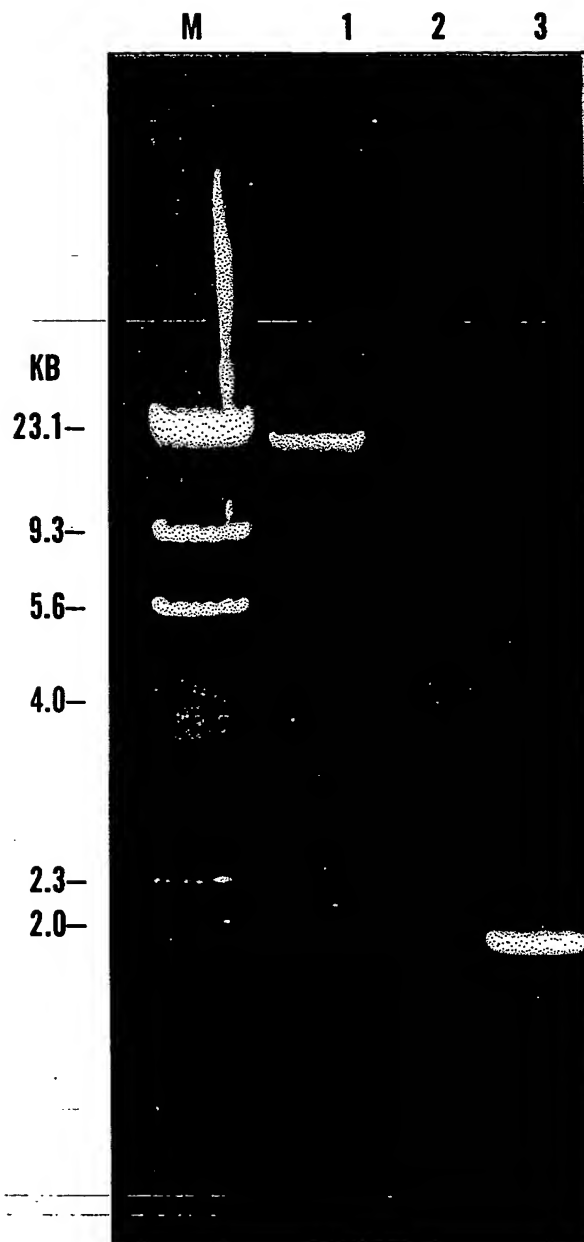


FIG. 4A

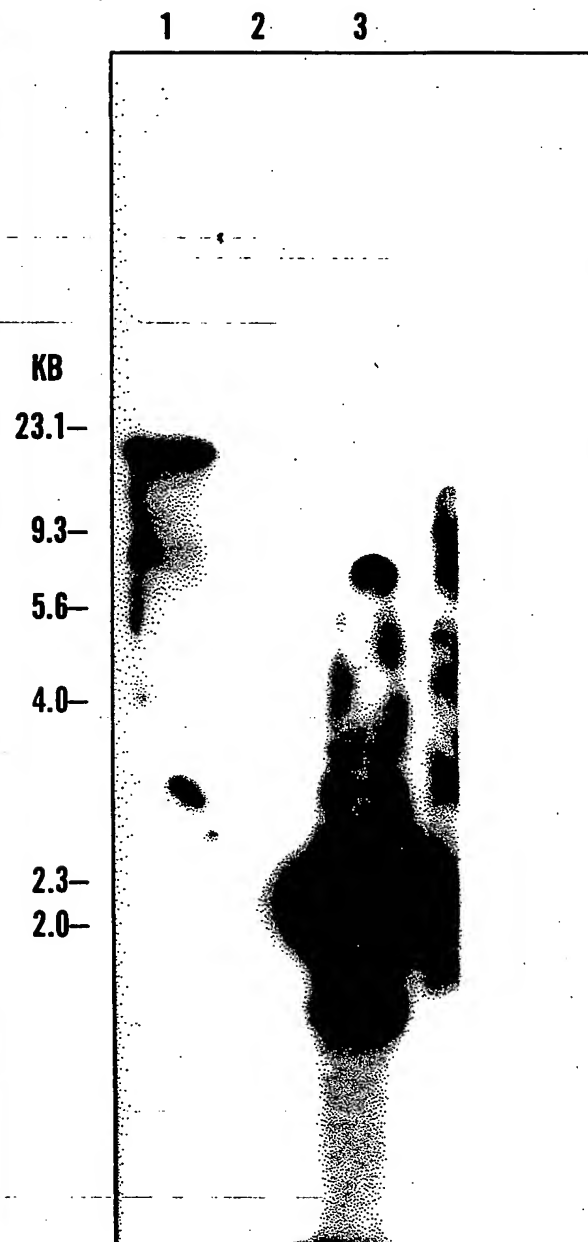


FIG. 4B

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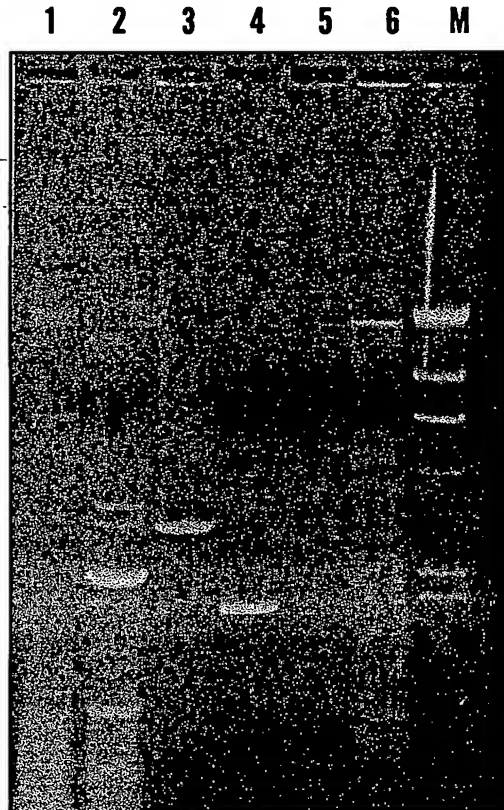


FIG. 5

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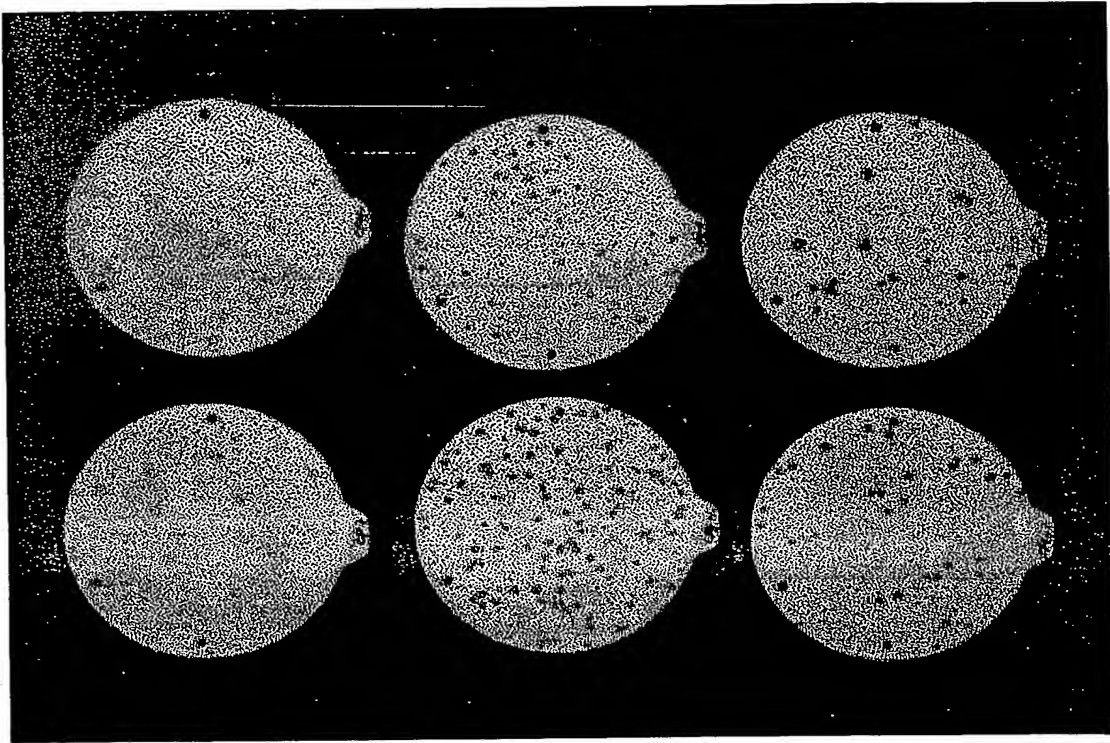


FIG. 6

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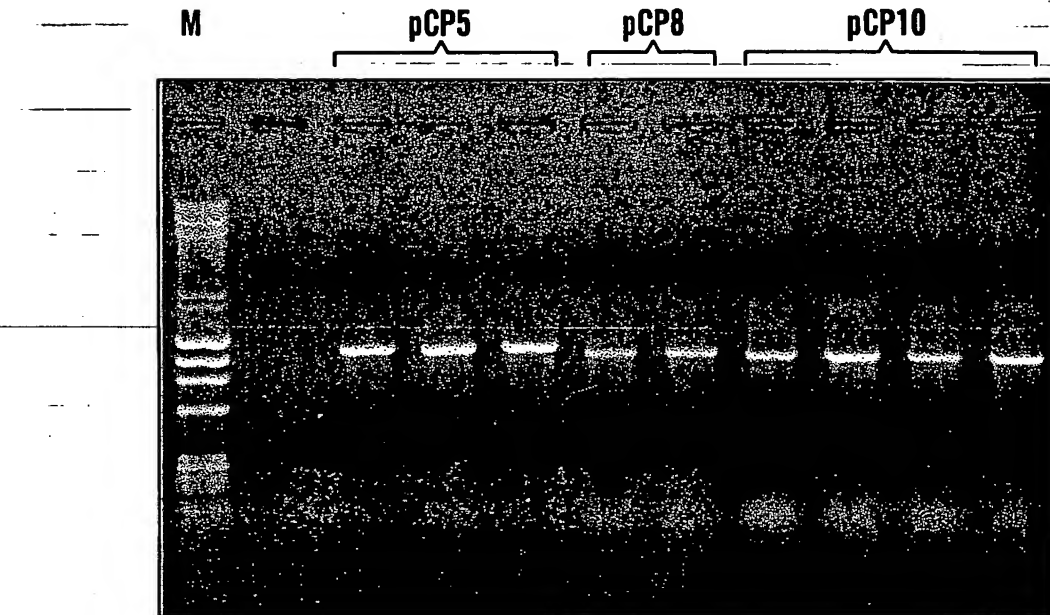


FIG. 7

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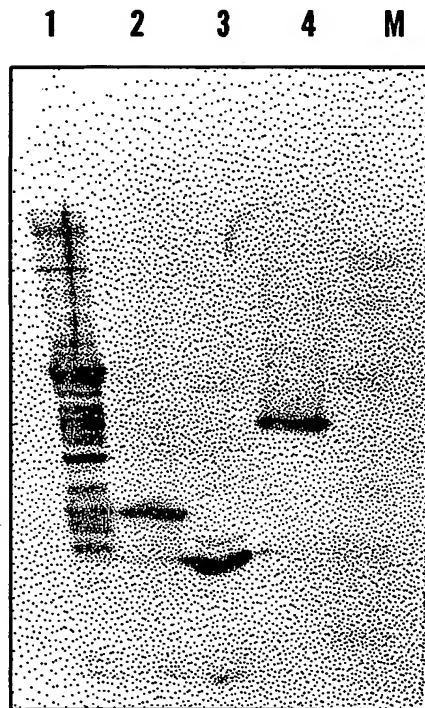


FIG. 8A

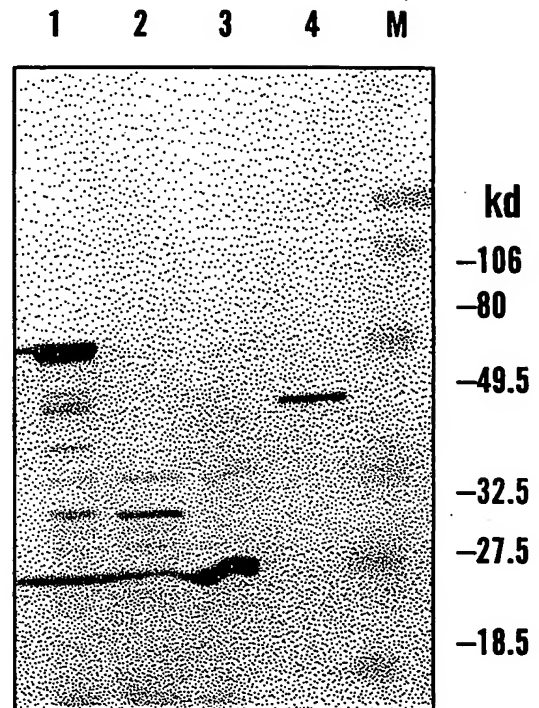


FIG. 8B

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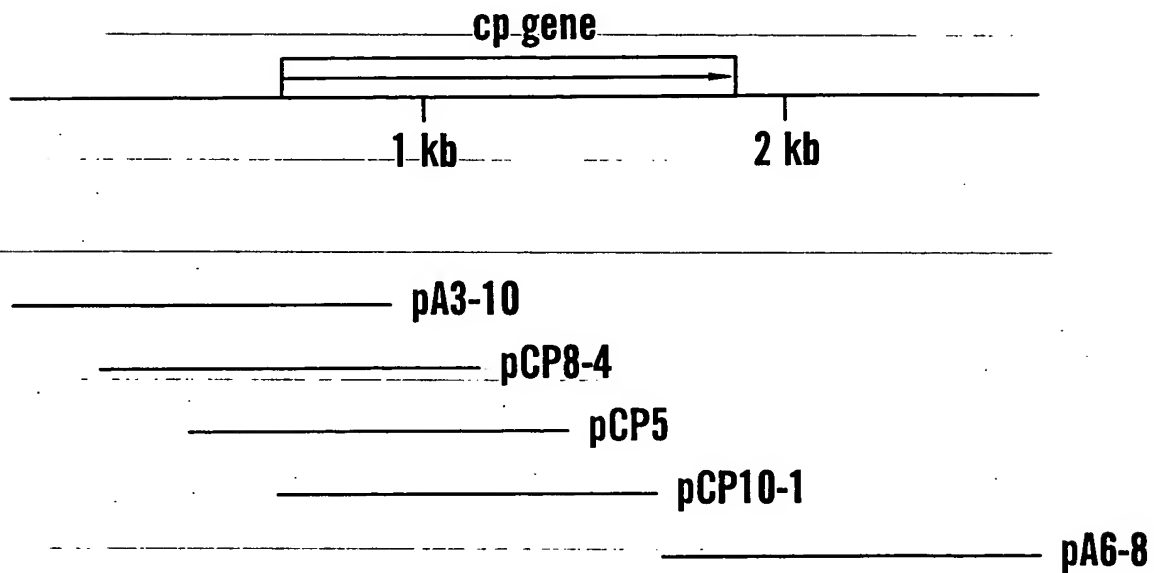


FIG. 9

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```
1  ATGGCATTGTGAACCTGAAATTTAGGGCAGATATATGAAGTCGTCCCCGAAAATAATTTGAGA 60
  M A F E L K L G Q I Y E V V P E N N L R -
61  GTTAGAGTGGGGGATGCGGCACAAGGAAAATTTAGTAAGGCGAGTTTCTTAAAGTACGTT 120
  V R V G D A A Q G K F S K A S F L K Y V -
121 AAGGACGGGACACAGGCGGAATTAACGGGAATCGCCGTAGTGCCCGAAAAATACGTATTC 180
  K D G T Q A E L T G I A V V P E K Y V F -
181 GCCACAGCAGCTTTGGCTACAGCGGCGCAGGAGCCACCTAGGCAGCCACCAGCGCAAGTG 240
  A T A A L A T A A Q E P P R Q P P A Q V -
241 GCGGAACCACAGGAAACCGATATAGGGGTAGTGCCGGAATCTGAGACTCTCACACCAAAT 300
  A E P Q E T D I G V V P E S E T L T P N -
301 AAGTTGGTTTTCGAGAAAGATCCAGACAAGTTCTTGAAGACTATGGGCAAGGGAATAGCT 360
  K L V F E K D P D K F L K T M G K G I A -
361 TTGGACTTGGCGGGAGTTACCCACAAACCGAAAGTTATTAACGAGCCAGGGAAAGTATCA 420
  L D L A G V T H K P K V I N E P G K V S -
421 GTAGAGGTGGCAATGAAGATTAATGCCGCATTGATGGAGCTGTGTAAGAAGGTTATGGGC 480
  V E V A M K I N A A L M E L C K K V M G -
481 GCCGATGACGCAGCAACTAAGACAAAATTCCTTCTGTACGTGATGCAGATTGCTTGCACG 540
  A D D A A T K T K F F L Y V M Q I A C T -
541 TTCTTTACATCGTCTTCGACGGAGTTCAAAGAGTTTGAAGTACATAGAAACCGATGATGGA 600
  F F T S S S T E F K E F D Y I E T D D G -
601 AAGAAGATATATGCGGTGTGGGTATATGATTGCATTAAACAAGCTGCTGCTTCGACGGGT 660
  K K I Y A V W V Y D C I K Q A A A S T G -
661 TATGAAAACCCGGTAAGGCAGTATCTAGCGTACTTCACACCAACCTTCATCAGGGCGACC 720
  Y E N P V R Q Y L A Y F T P T F I T A T -
721 CTGAATGGTAAACTAGTGATGAACGAGAAGGTTATGGCACAGCATGGAGTACCACCGAAA 780
  L N G K L V M N E K V M A Q H G V P P K -
781 TTCTTTCCGTACACGATAGACTGCGTTCGTCCGACGTACGATCTGTTCAACAACGACGCA 840
  F F P Y T I D C V R P T Y D L F N N D A -
841 ATATTAGCATGGAATTTAGCTAGACAGCAGGCGTTTAGAAACAAGACGGTAACGGCCGAT 900
  I L A W N L A R Q Q A F R N K T V T A D -
901 AACACCTTACACAACGTCTTCCAACCTATTGCAAAAGAAGTAG 942
  N T L H N V F Q L L Q K K *
```

FIG. 10

	1				50
BYV_CP
CTV_CP
LIYV_CP
GLRaV3_CP	MAFELKLGQI	YEVVPENNLR	VRVGDAAQGK	FSKASFLKYV	KDGTQAEALTG
CONSENSUS	-----	-----	-----	-----	-----
	51				100
BYV_CP
CTV_CP	MDDETKKLKN
LIYV_CP	MDTDGD	NDVFGSGNDT	RNNDDKKKEE	MKQNISDNSQ
GLRaV3_CP	IAVVPEKYVF	ATAALATAAQ	EPPRQPPAQV	AEPQETDIGV	VPESETLTPN
CONSENSUS	-----	-----	-----	-----	-----
	101				150
BYV_CPMGSAE	PISAIA..TF	ENVSL.AD.Q	TCLHGEDCDK	LRK.....N
CTV_CP	KNKETKEGDD	VVAAES..SF	GSVNLHID.P	TLITMNDVRQ	LSTQQNAALN
LIYV_CP	IISTRDHEAD	IIGSISKEDL	SKIVVRVDRH	DALSANDVQS	FR...EAMIN
GLRaV3_CP	KLVFEKDPDK	FLKTMGKGIA	LDLAGVTHKP	KVI..NEPGK	VSVEVAMKIN
CONSENSUS	-----d	-i-----f	--v----d--	-----nd---	1-----N
	151				200
BYV_CP	FEECLKLKG.	...VPEDNLG	IALGLCLYSC	AT.IGTSNKV	NVQPTS.TFI
CTV_CP	RDLFLALKGK	YPNLPDKDKD	FHIAMMLYRL	AV.KSSSLQS	DDDTTGITYT
LIYV_CP	...FMRDKDP	NRNQPSDKLI	IAMEVGVIYQM	VINLGTSAKL	G.NANNLEFT
GLRaV3_CP	.AALMELCKK	VMGADDAATK	TKFFLYVMQI	ACTFFTS..S	STEFKEFDYI
CONSENSUS	---f--lk--	----pd----	----l--y--	a----tS---	-----
	201				250
BYV_CP	KASFGGKEL	YLTHGELNSF	LGSQKLLEGK	PNKLRCFCRT	FQKDYISLRK
CTV_CP	R....EGVEV	DLSDKLWTDI	VYNSKGIGNR	TNALRVWGRT	NDALYLAFCR
LIYV_CP	IAYDQETR TY	KVAD..FVNY	MQSR..MRNS	PNVVRQYARA	MEKTINNIRS
GLRaV3_CP	ET..DDGKKI	Y..AVWVYDC	IKQAAASTGY	ENPVRQYLA Y	FTPFTITATL
CONSENSUS	-----eg---	-----	-----	-N--R-y-r-	----y-----
	251				300
BYV_CP	EYRGKLPPIA	RANRHGLPAE	DHYLAADF.I	STSTELTDLQ	QSRLLLAREN
CTV_CP	QNR.NLSYGG	RPLDAGIPAG	YHYLCADF.L	.TGAGLTDLE	CAVYIOAKEQ
LIYV_CP	AGIIN.SNGV	LAAKHGVLAS	YRNSYSDFAV	GFGNDTTDAQ	LTSMLLARKQ
GLRaV3_CP	NGKLV MNEKV	MA.QHGVPPK	FFPYTIDCVR	PTYDLFNND A	ILAWNLARQQ
CONSENSUS	-----l----	-a--hGvpa-	y-----Df--	-t---ltd--	-----lAr-q
	301				328
BYV_CP	ATH.TEFSSE	SPVTSCLKQLG	RGLGTGR*		
CTV_CP	LLK.KRGAD E	VVVTNVRQLG	K.FNTR*.		
LIYV_CP	ALC.KGEGGS	VEHYNTMQLA	NLKHPC*.		
GLRaV3_CP	AFRNKTVTAD	NTLHNVFQLL	QKK*....		
CONSENSUS	al--k----e	----n--QL-	-----		

FIG. 11

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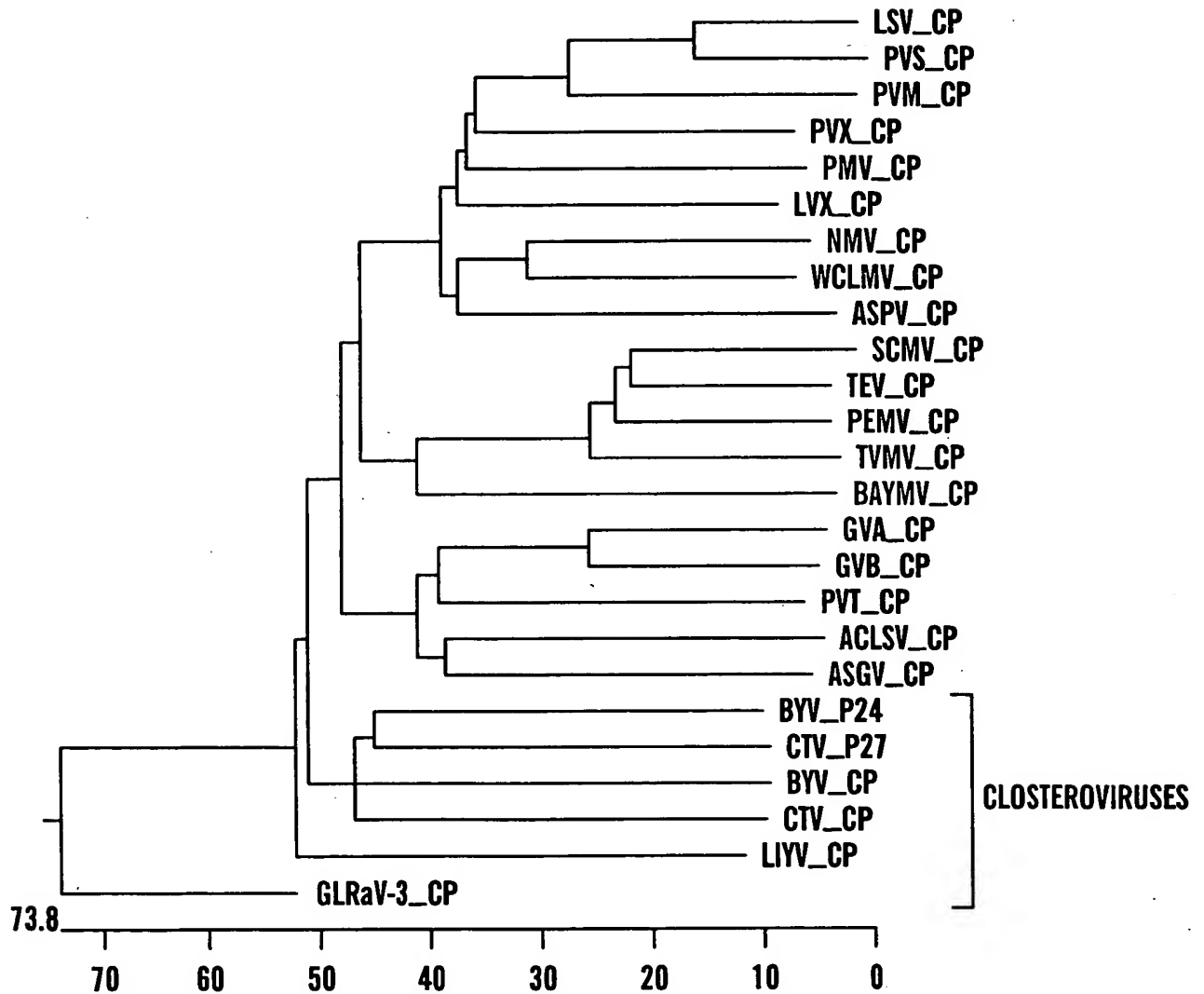


FIG. 12

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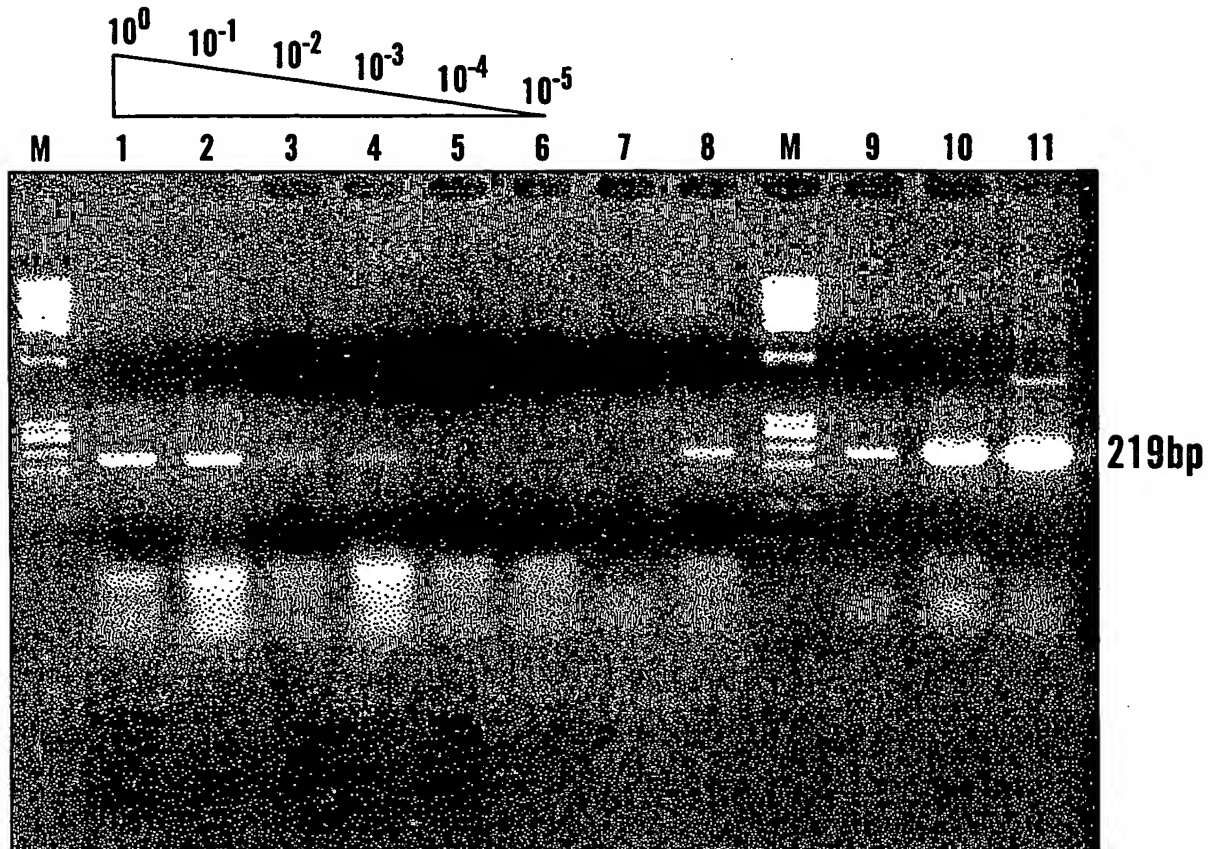


FIG. 13

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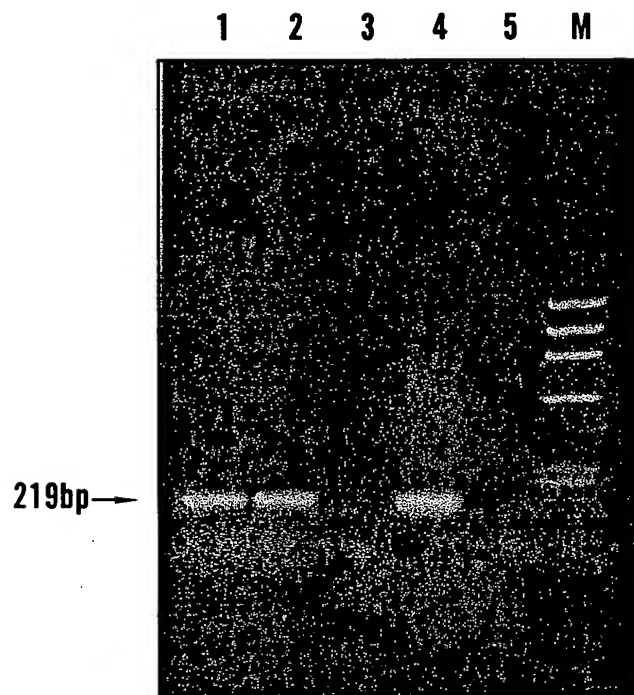


FIG. 14

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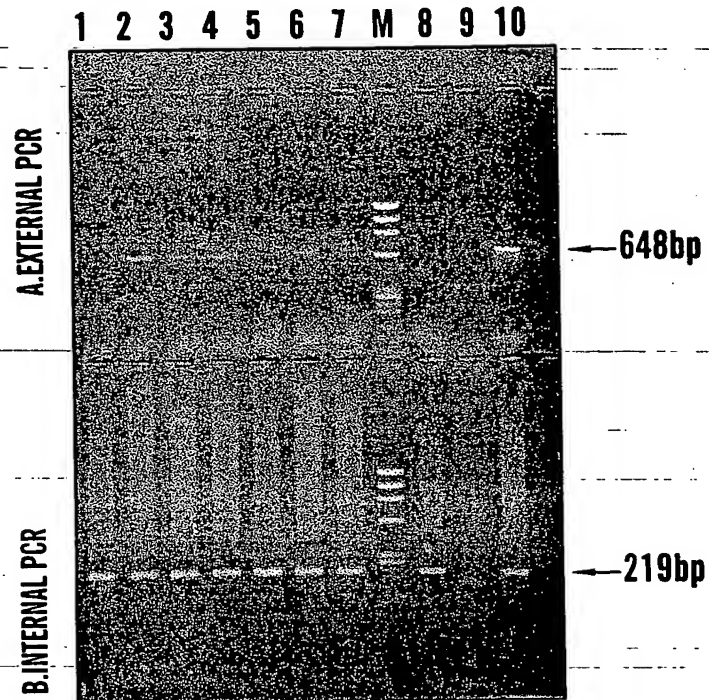


FIG. 15

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A. PK NESTED PCR

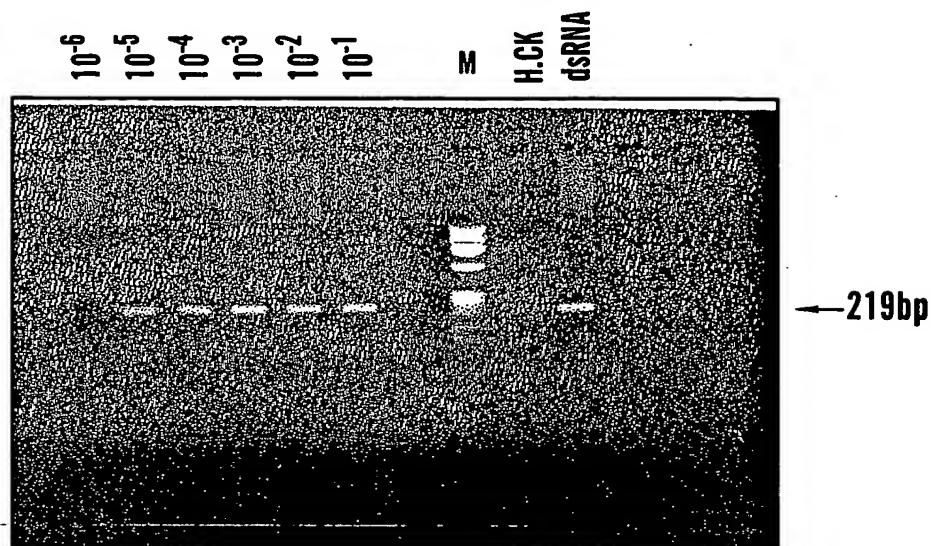


FIG. 16A

B. IC NESTED PCR

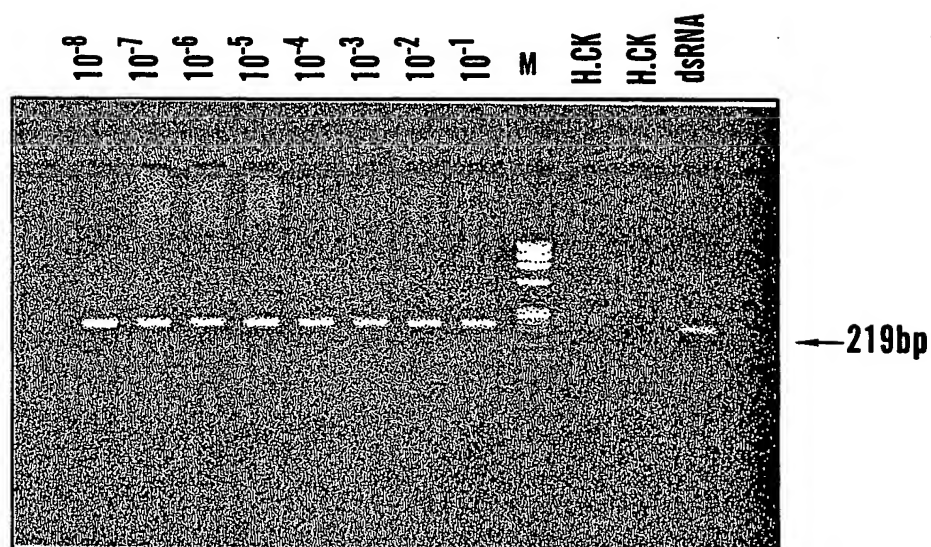


FIG. 16B



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FIG. 18A

ORF1a (HELICASE)

GTGTCTACTTACGCGAAGAGTGTGATGAACGACAATTTCAATATCCTTGAGACCCTGGTA
1 -----+-----+-----+-----+-----+-----+ 60
CACAGATGAATGCGCTTCTCAGCTACTTGTGTTAAAGTTATAGGAACTCTGGGACCAT
a V S T Y A K S V M N D N F N I L E T L V -

ACTTTGCCCAAGTCCTTTATAGTCAAAGTACCTGGTTCGGTGTGCTGGTTAGCATAACCACT
61 -----+-----+-----+-----+-----+-----+ 120
TGAAACGGGTTTCAGGAAATATCAGTTTCATGGACCAAGCCACGACCAATCGTATTGGTGA
a T L P K S F I V K V P G S V L V S I T T -

TCGGGCATTTCCGACAACTTGAAGTTCGGGGCGCGTTCGACGTTTCTAAAAAGAATTTCT
121 -----+-----+-----+-----+-----+-----+ 180
AGCCCGTAAAGGCTGTTTGAAGTTCGAGCCCGCGCAAGCTGCAAGATTTTCTTAAAG
a S G I S D K L E L R G A F D V S K K N F -

TCCAGGAGGTTACGTTTCGAGTCGTTTGC GCGTATTTTCTAGGGCTATTGTGGAGGATACG
181 -----+-----+-----+-----+-----+-----+ 240
AGGTCCTCCAATGCAAGCTCAGCAAACGCGCATAAAAGATCCCGATAACACCTCCTATGC
a S R R L R S S R L R V F S R A I V E D T -

ATCAAGGTTATGAAGGGCATGAAATCAGAGGATGGTAAACCACTCCCTATAGCCGAGGAT
241 -----+-----+-----+-----+-----+-----+ 300
TAGTTCCAATACTTCCCGTACTTTAGTCTCTCTACCATTGTTGGTGAGGGATATCGGCTCCTA
a I K V M K G M K S E D G K P L P I A E D -

TCCGTGTACGCGTTCATGACAGGCAATATGTCAAACGTTTCATTGCACTAGGGCTGGTTTG
301 -----+-----+-----+-----+-----+-----+ 360
AGGCACATGCGCAAGTACTGTCCGTTTATACAGTTTGCAAGTAACGTGATCCCGACCAAAC
a S V Y A F M T G N M S N V H C T R A G L -

CTCGGGGGCTCAAAGGCTTGC GCGGCTTCTTTAGCTGTGAAGGGTGCAGCTTCACGCGCT
361 -----+-----+-----+-----+-----+-----+ 420
GAGCCCCCGAGTTTCCGAACGCGCCGAAGAAATCGACACTTCCCACGTGCAAGTGCGCGA
a L G G S K A C A A S L A V K G A A S R A -

ACTGGAACAAACTCTTTTCAGGTCTCACATCCTTTCTTTCCGCCGGTGGTCTGTTTTAC
421 -----+-----+-----+-----+-----+-----+ 480
TGACCTTGTTTTGAGAAAAGTCCAGAGTGTAGGAAAGAAAGGCGGCCACCAGACAAAATG
a T G T K L F S G L T S F L S A G G L F Y -

GATGAAGGCTTGACGCCCCGAGAGAGGCTTGATGCACTAACGCGCCGTGAACATGCTGTG
481 -----+-----+-----+-----+-----+-----+ 540
CTACTTCCGAAGTGC GGGCTCTCTCCGAAGTACGTGATTGCGCGGCACTTGTACGACAC
a D E G L T P G E R L D A L T R R E H A V -

AATTCACCTGTAGGCTCTTAGAACCTGGAGCTTCGGTTGCGAAGCGGGTCTGTTCCGGA
541 -----+-----+-----+-----+-----+-----+ 600
TTAAGTGGACATCCGGAATCTTGGACCTCGAAGCCAACGCTTCGCCCAGCAAAGGCTT
a N S P V G L L E P G A S V A K R V V S G -

ACGAAAGCTTTTCTGTCAGAATTGTCATTGGAGGACTTCACCACTTTTCGTCATAAAAAAT
601 -----+-----+-----+-----+-----+-----+ 660
TGCTTTCGAAAAGACAGTCTTAACAGTAACCTCCTGAAGTGGTGAAAGCAGTATTTTAA
a T K A F L S E L S L E D F T T F V I K N -

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FIG. 18B

```
AGGGTGCTTATTGGTGTGTTTTACTCTTTCCATGGCTCTCACTCCGGTGGTCTGGAAGTAC
661 -----+-----+-----+-----+-----+-----+-----+ 720
TCCCACGAATAACCACAAAATGAGAAAGGTACCGAGAGTGAGGCCACCAGACCTTCATG
a R V L I G V F T L S M A L T P V V W K Y -

AGAAGGAATATCGCGCGAACTGGCGTGATGTTTTCCACCGTGCTCGTTCCGGGTACCGCG
721 -----+-----+-----+-----+-----+-----+-----+ 780
TCTTCCTTATAGCGCGCTTGACCGCACCTACAAAGGTGGCAGCAGCAAGCCCATGGCGC
a R R N I A R T G V D V F H R A R S G T A -

GCCATCGGTTTACAATGTCTTAGTGAGGAAGGTCGTTAGCTGGTGACGCTGCTCGTGGC
781 -----+-----+-----+-----+-----+-----+-----+ 840
CGGTAGCCAAATGTTACAGAATCACCTCCTTCCAGCAATCGACCACTGCGACGAGCACCG
a A I G L Q C L S G G R S L A G D A A R G -

GCGTTAACAGTGA CTGAGGAGGGCTATCTTCGGCGGTTGCGGTGACCAGAAATACAGTG
841 -----+-----+-----+-----+-----+-----+-----+ 900
CGCAATTGTCACTGAGCTCCTCCCGATAGAAGCCGCCAACGCCACTGGTCTTTATGTCAC
a A L T V T R G G L S S A V A V T R N T V -

GCTAGGCGTCAGGTACCATTGGCGTGTCTTTTCGTTTTCCACGTCTTACGCAGTCAGTGGT
901 -----+-----+-----+-----+-----+-----+-----+ 960
CGATCCGCAGTCCATGGTAACCGCAACGAAAGCAAAAGGTGCAGAATGCGTCAGTCACCA
a A R R Q V P L A L L S F S T S Y A V S G -

TGCACTTTGTTAGGTATTTGGGCTCATGCTCTCCCTAGGCATTTGATGTTCTTCTTTGGC
961 -----+-----+-----+-----+-----+-----+-----+ 1020
ACGTGAAACAATCCATAAACCCGAGTACGAGAGGGATCCGTAAACTACAAGAAGAAACCG
a C T L L G I W A H A L P R H L M F F F G -

CTAGGGACGCTCTTCGGGGTGAGTGCCAGTACCAATTCTTGGTCGCTTGGGGGCTATACG
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
GATCCCTGCGAGAAGCCCCACTCACGGTCATGGTTAAGAACCAGCGAACCCCCGATATGC
a L G T L F G V S A S T N S W S L G G Y T -

AACAGTCTGTTACCGTACCGGAATTAAGTTGGGAAGGAGGAGTTACAGATCTTTATTG
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
TTGTCAGACAAGTGGCATGGCCTTAATTGAACCTTCCCTCCTCAATGTCTAGAAATAAC
a N S L F T V P E L T W E G R S Y R S L L -

CCCCAAGCAGCTTTAGGTATTTCTCTCGTTGTGCGGGGTGTTAAGTGAAACTGTGCCA
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
GGGGTTCGTCGAAATCCATAAAGAGAGCAACACGCGCCCAACAATTCACCTTTGACACGGT
a P Q A A L G I S L V V R G L L S E T V P -

CAACTAACGTACGTACCGCCGATTGAAGGTCCGAATGTTTATGATCAGGCACTAAATTTT
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
GTTGATTGCATGCATGGCGGCTAACTTCCAGCCTTACAAATACTAGTCCGTGATTTAAAA
a Q L T Y V P P I E G R N V Y D Q A L N F -

TATCGCGACTTTGACTATGACGATGGTGCAGGCCCATCCGGGACGGCTGGTCAAAGCGAT
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
ATAGCGCTGAAACTGATACTGCTACCACGTCCGGGTAGGCCCTGCCGACCAGTTTCGCTA
a Y R D F D Y D D G A G P S G T A G Q S D -
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FIG. 18C

1321 CCTGGAACCAATACTTCGGATACTTCTTCGGTTTTCTCTGACGATGGTTTGCCCGCTAGT
-----+-----+-----+-----+-----+-----+ 1380
GGACCTTGGTTATGAAGCCTATGAAGAAGCCAAAAGAGACTGCTACCAAACGGGCGATCA
a P G T N T S D T S S V F S D D G L P A S -

1381 GGCGGTGGCTTCGACGCGCGCGTTGAGGCAGGTCCCAGCCATGCTGTTGATGAATCACCA
-----+-----+-----+-----+-----+-----+ 1440
CCGCCACCGAAGCTGCGCGCGCAACTCCGTCCAGGGTCGGTACGACAACACTACTTAGTGGT
a G G G F D A R V E A G P S H A V D E S P -

1441 AGGGGTAGTGTGAGTTCGTCTACAGAGAACGTGTAGATGAACATCCGGCGTGTGGTGAA
-----+-----+-----+-----+-----+-----+ 1500
TCCCCATCACAACCTCAAGCAGATGTCTCTTGACATCTACTTGTAGGCCGCACACCACTT
a R G S V E F V Y R E R V D E H P A C G E -

1501 GCTGAAGTTGAAAAGGATCTAATAACACCACTTGGTACAGCTGTCTTAGAGTCGCCCCC
-----+-----+-----+-----+-----+-----+ 1560
CGACTTCAACTTTTCCTAGATTATTGTGGTGAACCATGTGACAGAATCTCAGCGGGGGG
a A E V E K D L I T P L G T A V L E S P P -

1561 GTAGGTCCTGAAGCTGGGAGCGCGCCCAACGTCGAGGACGGTTGTCCGGAGGTTGAAGCT
-----+-----+-----+-----+-----+-----+ 1620
CATCCAGGACTTCGACCCTCGCGCGGGTTGCAGCTCCTGCCAACAGGCCTCCAACCTCGA
a V G P E A G S A P N V E D G C P E V E A -

1621 GAGAAATGTTTCGGAGGTCATCGTTGACGTTCTTAGTTTCAAGACCGCCGGTACAAGAAGTC
-----+-----+-----+-----+-----+-----+ 1680
CTCTTTACAAGCCTCCAGTAGCAACTGCAAGGATCAAGTCTTGGCGGCCATGTTCTTCAG
a E K C S E V I V D V P S S E P P V Q E V -

1681 CTTGAATCAACCAATGGTGTCCAAGCTGCAAGAACTGAAGAGGTTGTGCAGGGCGACACA
-----+-----+-----+-----+-----+-----+ 1740
GAACTTAGTTGGTTACCACAGGTTTCGACGTTCTTGAAGTCTTCCAACACGTCCCGCTGTGT
a L E S T N G V Q A A R T E E V V Q G D T -

1741 TGTGGAGCTGGGGTAGCTAAATCAGAAGTGAGTCAACGTGTGTTTCTGCGCAAGTACCC
-----+-----+-----+-----+-----+-----+ 1800
ACACCTCGACCCCATCGATTAGTCTTCACTCAGTTGCACACAAAGGACGCGTTCATGGG
a C G A G V A K S E V S Q R V F P A Q V P -

1801 GCACATGAAGCTGGTCTTGAGGCATCTAGTGGCGCGGTGCGTGGAGCCATTGCAAGTTTCT
-----+-----+-----+-----+-----+-----+ 1860
CGTGTACTTCGACCAGAAGTCCGTAGATCACCGCGCCAGCACCTCGGTAACGTTCAAAGA
a A H E A G L E A S S G A V V E P L Q V S -

1861 GTGCCAGTAGCCGTAGAGAAAAGTGTCTTATCTGTGCGAGAAGGCGCGTGAGCTAAAGCGC
-----+-----+-----+-----+-----+-----+ 1920
CACGGTCATCGGCATCTCTTTGACAAAATAGACAGCTCTTCCGCGCACTCGATTTCGCG
a V P V A V E K T V L S V E K A R E L K A -

1921 GTAGATAAGGGCAAGGCGGTGCGTGCACGCAAAGGAAGTCAAGAATGTACCGGTTAAGACG
-----+-----+-----+-----+-----+-----+ 1980
CATCTATTCCTCGTCCGCCAGCACGTGCGTTTCTTCACTTCTTACATGGCCAATTCTGC
a V D K G K A V V H A K E V K N V P V K T -

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FIG. 18D

1981 TTACCACGAGGGGCTCTAAAAATTAGTGAGGATACCGTTCGTAAGGAATTGTGCATGTTT
-----+-----+-----+-----+-----+-----+ 2040
AATGGTGCTCCCGAGATTTTAACTACTCCTATGGCAAGCATTCTTAACACGTACAAA
a L P R G A L K I S E D T V R K E L C M F -

2041 AGAACGTGTTCTGCGGCGTGACGTTGGACGTGTACAATGAAGCGACCATCGCCACTAGG
-----+-----+-----+-----+-----+-----+ 2100
TCTTGACAAGGACGCCGCACGTCAACCTGCACATGTTACTTCGCTGGTAGCGGTGATCC
a R T C S C G V Q L D V Y N E A T I A T R -

2101 TTCTCAAATGCGTTTACCTTTGTTCGATAGCTTGAAAGGGAGGAGTGCGGTCTTTTTCTCA
-----+-----+-----+-----+-----+-----+ 2160
AAGAGTTTACGCAAATGGAAACAGCTATCGAACTTTCCCTCCTCAGCCAGAAAAAGAGT
a F S N A F T F V D S L K G R S A V F F S -

2161 AAGCTGGGTGAGGGGTATACCTATAATGGTGGTAGCCATGTTTCATCAGGGTGGCCTCGT
-----+-----+-----+-----+-----+-----+ 2220
TTCGACCCACTCCCATATGGATATTACCACCATCGGTACAAAGTAGTCCCACCGGAGCA
a K L G E G Y T Y N G G S H V S S G W P R -

2221 GCCCTAGAGGATATCTTAACGGCAATTAAGTACCCAAGCGTCTTCGACCACTGTTTAGTG
-----+-----+-----+-----+-----+-----+ 2280
CGGGATCTCCTATAGAATTGCCGTTAATTCATGGGTTCGAGAAGCTGGTGACAAATCAC
a A L E D I L T A I K Y P S V F D H C L V -

2281 CAGAAGTACAAGATGGGTGGAGGCGTACCATTCCACGCTGATGACGAGGAGTGCTATCCA
-----+-----+-----+-----+-----+-----+ 2340
GTCTTCATGTTCTACCCACCTCCGCATGGTAAGGTGCGACTACTGCTCCTCAGGATAGGT
a Q K Y K M G G G V P F H A D D E E C Y P -

2341 TCAGATAACCCTATCTTGACGGTCAATCTCGTGGGGAAGGCAAACTTCTCGACTAAGTGC
-----+-----+-----+-----+-----+-----+ 2400
AGTCTATTGGGATAGAAGTGCAGTTAGAGCACCCCTTCCGTTTGAAGAGCTGATTCACG
a S D N P I L T V N L V G K A N F S T K C -

2401 AGGAAGGGTGGTAAGGTCATGGTCATAAACGTAGCTTCGGGTGACTATTTTCTTATGCCT
-----+-----+-----+-----+-----+-----+ 2460
TCCTTCCCACCATTCAGTACCAGTATTTGCATCGAAGCCCACTGATAAAAGAATACGGA
a R K G G K V M V I N V A S G D Y F L M P -

2461 TGCGGTTTTCAAAGGACGCACTTGCATTAGTAAACTCCATCGACGAAGGGCGCATCAGT
-----+-----+-----+-----+-----+-----+ 2520
ACGCCAAAAGTTTCTGCGTGAACGTAAGTCATTTGAGGTAGCTGCTTCCCGGTAGTCA
a C G F Q R T H L H S V N S I D E G R I S -

2521 TTGACGTTTCAGGGCAACTCGGCGCGTCTTTGGTGTAGGCAGGATGTTGCAGTTAGCCGGC
-----+-----+-----+-----+-----+-----+ 2580
AACTGCAAGTCCCGTTGAGCCGCGCAGAAACCACATCCGTCCTACAACGTCAATCGGCCG
a L T F R A T R R V F G V G R M L Q L A G -

2581 GGCGTGTGGATGAGAAGTCACCAGGTGTTCCAAACCAGCAACCACAGAGCCAAGGTGCT
-----+-----+-----+-----+-----+-----+ 2640
CCGCACAGCCTACTCTTCAAGTGGTCCACAAGGTTTGGTGGTGTCTCGGTTCCACGA
a G V S D E K S P G V P N Q Q P Q S Q G A -

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FIG. 18E

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2641 ACCAGAACAATCACACCAAAATCGGGGGGCAAGGCTCTATCTGAGGGAAGTGGTAGGGAA
-----+-----+-----+-----+-----+-----+ 2700
a TGGTCTTGTTAGTGTGGTTTTAGCCCCCGTTCCGAGATAGACTCCCTTCACCATCCCTT
T R T I T P K S G G K A L S E G S G R E -

2701 GTCAAGGGGAGGTCGACATACTCGATATGGTGCGAACAAGATTACGTTAGGAAGTGTGAG
-----+-----+-----+-----+-----+-----+ 2760
a CAGTTCCCCTCCAGCTGTATGAGCTATAACCACGCTTGTTCATGAATCCTTCACACTC
V K G R S T Y S I W C E Q D Y V R K C E -

2761 TGGCTCAGGGCTGATAATCCAGTGATGGCTCTTRAACCTGGCTACACCCCAATGACATTT
-----+-----+-----+-----+-----+-----+ 2820
a ACCGAGTCCCGACTATTAGGTCACCTACCGAGAAAYTTGGACCGATGTGGGGTTACTGTAAA
W L R A D N P V M A L ? P G Y T P M T F -

2821 GAAGTGGTTAAAGCCGGGACCTCTGAAGATGCCGTCGTGGAGTACTTGAAGTATCTGGCT
-----+-----+-----+-----+-----+-----+ 2880
a CTTACCAATTTTCGGCCCTGGAGACTTCTACGGCAGCACCTCATGAAGTTCATAGACCGA
E V V K A G T S E D A V V E Y L K Y L A -

2881 ATAGGCATTGGGAGGACATACAGGGCGTTGCTTATGGCTAGAAATATTGCCGTCACCTACC
-----+-----+-----+-----+-----+-----+ 2940
a TATCCGTAACCTCCTGTATGTCCCGCAACGAATACCGATCTTTATAACGGCAGTGATGG
I G I G R T Y R A L L M A R N I A V T T -

2941 GCCGAAGGTGTTCTGAAAGTACCTAATCAAGTTTATGAATCACTACCGGGCTTTCACGTT
-----+-----+-----+-----+-----+-----+ 3000
a CGGCTTCCACAAGACTTTCATGGATTAGTTCAAATACTTAGTGATGGCCCCGAAAGTGCAA
A E G V L K V P N Q V Y E S L P G F H V -

3001 TACAAGTCGGGCACAGATCTCATTTTTTCATTCAACACAAGACGGCTTGCGTGTGAGAGAC
-----+-----+-----+-----+-----+-----+ 3060
a ATGTTACAGCCCGTGTCTAGAGTAAAAAGTAAGTTGTGTTCTGCCGAACGCACACTCTCTG
Y K S G T D L I F H S T Q D G L R V R D -

3061 CTACCGTACGTATTCATAGCTGAGAAAGGTATTTTTATCAAGGGCAAAGATGTCGACGCG
-----+-----+-----+-----+-----+-----+ 3120
a GATGGCATGCATAAGTATCGACTCTTTCCATAAAAAATAGTTCCCGTTTCTACAGCTGCGC
L P Y V F I A E K G I F I K G K D V D A -

3121 GTAGTAGCTTTGGGCGACAATCTGTCCGTATGTGATGATATATTGGTTTTCCATGATGCT
-----+-----+-----+-----+-----+-----+ 3180
a CATCATCGAAACCCGCTGTTAGACAGGCATACACTACTATATAACCAAAGGTACTACGA
V V A L G D N L S V C D D I L V F H D A -

3181 ATTAATTTGATGGGTGCACTGAAAGTTGCTCGATGTGGTATGGTGGGTGAATCATTTAAG
-----+-----+-----+-----+-----+-----+ 3240
a TAATTAACTACCCACGTGACTTTCAACGAGCTACACCATACCACCCACTTAGTAAATTC
I N L M G A L K V A R C G M V G E S F K -

3241 TCGTTCGAATACAAATGCTATAATGCTCCCCCAGGTGGCGGTAAGACGACGATGCTAGTG
-----+-----+-----+-----+-----+-----+ 3300
a AGCAAGCTTATGTTTACGATATTACGAGGGGGTCCACCGCCATTCTGCTGCTACGATCAC
S F E Y K C Y N A P P G G G K T T M L V -

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FIG. 18F

3301 GACGAATTTGTCAAGTCACCCAATAGCACGGCCACCATTACGGCTAACGTGGGAAGTTCT
-----+-----+-----+-----+-----+-----+ 3360
CTGCTTAAACAGTTCAGTGGGTTATCGTGCCGGTGGTAATGCCGATTGCACCCTTCAAGA
a D E F V K S P N S T A T I T A N V G S S -

3361 GAGGACATAAATATGGCGGTGAAGAAGAGAGATCCGAATTTGGAAGGTCTCAACAGTGCT
-----+-----+-----+-----+-----+-----+ 3420
CTCCTGTATTTATACCGCCACTTCTTCTCTCTAGGCTTAAACCTTCCAGAGTTGTCACGA
a E D I N M A V K K R D P N L E G L N S A -

3421 ACCACAGTTAACTCCAGGGTGGTTAACTTTATTGTCAGGGGAATGTATAAAAGGGTTTTG
-----+-----+-----+-----+-----+-----+ 3480
TGGTGTCAATTGAGGTCCCACCAATTGAAATAACAGTCCCCTTACATATTTTCCCAAAC
a T T V N S R V V N F I V R G M Y K R V L -

3481 GTGGATGAGGTGTACATGATGCATCAAGGCTTACTACAACCTAGGCGTCTTCGCAACCGGC
-----+-----+-----+-----+-----+-----+ 3540
CACCTACTCCACATGTACTACGTAGTTCCGAATGATGTTGATCCGCAGAAGCGTTGGCCG
a V D E V Y M M H Q G L L Q L G V F A T G -

3541 GCGTCGGAAGGCCTCTTTTTTGGAGACATAAATCAGATACCATTTCATAAACMGGGAGAAG
-----+-----+-----+-----+-----+-----+ 3600
CGCAGCCTTCCGGAGAAAAACCTCTGTATTTAGTCTATGGTAAGTATTTGKCCCTCTTC
a A S E G L F F G D I N Q I P F I N R E K -

3601 GTGTTTAGGATGGATTGTGCTGTATTTGTTCCAAAGAAGGAAAGCGTTGTATACACTTCT
-----+-----+-----+-----+-----+-----+ 3660
CACAAATCCTACCTAACACGACATAAAACAAGGTTTCTTCCTTTCGCAACATATGTGAAGA
a V F R M D C A V F V P K K E S V V Y T S -

3661 AAATCATACAGGTGTCCGTTAGATGTTTGCTACTTGTGTCTCAATGACCGTAAGGGGA
-----+-----+-----+-----+-----+-----+ 3720
TTTAGTATGTCCACAGGCAATCTACAAACGATGAACAACAGGAGTTACTGGCATTCCCCT
a K S Y R C P L D V C Y L L S S M T V R G -

3721 ACGGAAAAGTGTTACCCTGAAAAGGTCGTTAGCGGTAAGGACAAACCAGTAGTAAGATCG
-----+-----+-----+-----+-----+-----+ 3780
TGCCTTTTCAATGGGACTTTTCCAGCAATCGCCATTCTGTTTGGTCATCATTCTAGC
a T E K C Y P E K V V S G K D K P V V R S -

3781 CTGTCCAAAAGGCCAATTGGAACCACTGATGACGTAGCTGAAATAAACGCTGACGTGTAC
-----+-----+-----+-----+-----+-----+ 3840
GACAGGTTTTCCGGTTAACCTTGGTGACTACTGCATCGACTTTATTTGCGACTGCACATG
a L S K R P I G T T D D V A E I N A D V Y -

3841 TTGTGCATGACCCAGTTGGAGAAGTCGGATATGAAGAGGTGCTTGAAGGGAAAAGGAAAA
-----+-----+-----+-----+-----+-----+ 3900
AACACGTACTGGGTCAACCTCTTCAGCCTATACTTCTCCAGCAACTTCCCTTTTCTTTT
a L C M T Q L E K S D M K R S L K G K G K -

3901 GAAACACCAGTGATGACAGTGCATGAAGCACAGGGAAAACATTTCAGTGATGTGGTATTG
-----+-----+-----+-----+-----+-----+ 3960
CTTTGTGGTCACTACTGTACGTACTTCGTGTCCCTTTTTGTAAGTCACTACACCATAAC
a E T P V M T V H E A Q G K T F S D V V L -

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FIG. 18G

3961 TTAGGACGAAGAAAGCCGATGACTCCCTATTCACTAAACAACCGCATATACTTGTGGT 4020
-----+-----+-----+-----+-----+-----+
a AAATCCTGCTTCTTTTCGGCTACTGAGGGATAAGTGATTGTGGCGTATATGAACAACCA
F R T K K A D D S L F T K Q P H I L V G -

4021 TTGTCGAGACACACACGCTCACTGGTTTATGCCGCTCTGAGCTCAGAGTTGGACGATAAG 4080
-----+-----+-----+-----+-----+-----+
a AACAGCTCTGTGTGTGCGAGTGACCAAATACGGCGAGACTCGAGTCTCAACCTGCTATTTC
L S R H T R S L V Y A A L S S E L D D K -
* A Q S W T I R -

(FRAMESHIFT)

4081 GTCGGCACATATATTAGCGACGCGTCGCTCAATCAGTATCCGACGCTTTGCTTCACACG 4140
-----+-----+-----+-----+-----+-----+
a CAGCCGTGTATATAATCGCTGCGCAGCGGAGTTAGTCATAGGCTGCCAAACGAAGTGTGC
V G T Y I S D A S P Q S V S D A L L H T -
S A H I L A T R H L N Q Y P T L C F T R -

ORF1b (RdRp)

4141 TTCGCCCCGGCTGGTTGCTTTTCGAGGTATATGAGCGTATGAATTTTGGACCGACCTTCGA 4200
-----+-----+-----+-----+-----+-----+
a AAGCGGGGCGCCGACCAACGAAAGCTCCATATACTCGCATACTTAAACCTGGCTGGAAGCT
F A P A G C F R G I * -
b S P R L V A F E V Y E R M N F G P T F E -

4201 AGGGGAGTTGGTACGGAAGATACCAACAAGTCATTTTGTAGCCGTGAATGGGTTTCTCGA 4260
-----+-----+-----+-----+-----+-----+
b TCCCCTCAACCATGCCTTCTATGGTTGTTTCAGTAAACATCGGCACTTACCCAAAGAGCT
G E L V R K I P T S H F V A V N G F L E -

4261 GGACTTACTCGACGGTTGTCCGGCTTTTCGACTATGACTTCTTTGAGGATGATTTCGAAAC 4320
-----+-----+-----+-----+-----+-----+
b CCTGAATGAGCTGCCAACAGGCCGAAAGCTGATACTGAAGAACTCCTACTAAAGCTTTG
D L L D G C P A F D Y D F F E D D F E T -

4321 TTCAGATCAGTCTTTCTCCTCATAGAAGATGTGCGCATTTCTGAATCTTTTTCTCATTTTGC 4380
-----+-----+-----+-----+-----+-----+
b AAGTCTAGTCAGAAAGGAGTATCTTCTACACGCGTAAAGACTTAGAAAAAGAGTAAACG
S D Q S F L I E D V R I S E S F S H F A -

4381 GTCGAAAATAGAGGATAGGTTTTACAGTTTTATTAGGTCTAGCGTAGGTTTACCAAAGCG 4440
-----+-----+-----+-----+-----+-----+
b CAGCTTTTATCTCCTATCCAAAATGTCAAATAATCCAGATCGCATCCAAATGGTTTCGC
S K I E D R F Y S F I R S S V G L P K R -

4441 CAACACCTTGAAGTGTAACCTCGTCACGTTTGAAAATAGGAATTCCAACGCCGATCGCGG 4500
-----+-----+-----+-----+-----+-----+
b GTTGTGGAACCTTCACATTGGAGCAGTGCAAACCTTTTATCCTTAAGGTTGCGGCTAGCGCC
N T L K C N L V T F E N R N S N A D R G -

4501 TTGTAACGTGGGTTGTGACGACTCTGTGGCGCATGAACTGAAGGAGATTTTCTTCGAGGA 4560
-----+-----+-----+-----+-----+-----+
b AACATTGCACCCAACACTGCTGAGACACCGCGTACTTGACTTCCTCTAAAAGAAGCTCCT
C N V G C D D S V A H E L K E I F F E E -

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FIG. 18H

4561 GGTCTTAACAAAGCTCGTTTAGCAGAGGTGACGGAAGCCATTTGTCCAGCAACACGAT
-----+-----+-----+-----+-----+-----+ 4620
CCAGCAATTGTTTCGAGCAAATCGTCTCCACTGCCTTTCGGTAAACAGGTCGTTGTGCTA
b V V N K A R L A E V T E S H L S S N T M -

4621 GTTGTATATCAGATTGGTTGGACAAAAGGGCACCTAACGCTTACAAGTCTCTCAAGCGGGC
-----+-----+-----+-----+-----+-----+ 4680
CAACAATAGTCTAACCAACCTGTTTTCCCGTGGATTGCGAATGTTTCAGAGAGTTCGCCCG
b L L S D W L D K R A P N A Y K S L K R A -

4681 TTTAGGTTTCGGTTGTCTTTTCATCCGCTCTATGTTGACGCTCTTATACGCTCATGGTGAAAGC
-----+-----+-----+-----+-----+-----+ 4740
AAATCCAAGCCAACAGAAAGTAGGCAGATACAACCTGCAGAATATGCGAGTACCACTTTTCG
b L G S V V F H P S M L T S Y T L M V K A -

4741 AGACGTAAAACCCAAGTTGGACAATACGCCATTGTGCAAGTACGTAACGGGGCAGAATAT
-----+-----+-----+-----+-----+-----+ 4800
TCTGCATTTTGGGTTCAACCTGTTATGCGGTAACAGCTTCATGCATTGCCCGCTCTTATA
b D V K P K L D N T P L S K Y V T G Q N I -

4801 AGTCTACCACGATAGGTGCGTAACTGCGCTTTTTTCTTGCAATTTTACTGCGTGCGTAGA
-----+-----+-----+-----+-----+-----+ 4860
TCAGATGGTGCTATCCACGCATTGACGCGAAAAAGAACGTAAAAATGACGCACGCATCT
b V Y H D R C V T A L F S C I F T A C V E -

4861 GCGCTTAAAATACGTAGTGGACGAAAGGTGGCTCTTCTACCACGGGATGGACACTGCGGA
-----+-----+-----+-----+-----+-----+ 4920
CGCGAATTTTATGCATCACCTGCTTTCCACCGAGAAGATGGTGCCCTACCTGTGACGCCT
b R L K Y V V D E R W L F Y H G M D T A E -

4921 GTTGGCGGCTGCATTGAGGAACAATTTGGGGGACATCCGGCAATACTACACCTATGAACT
-----+-----+-----+-----+-----+-----+ 4980
CAACCGCCGACGTAACCTCCTTGTTAAACCCCTGTAGGCCGTTATGATGTGGATACTTGA
b L A A A L R N N L G D I R Q Y Y T Y E L -

4981 GGATATCAGTAAGTACGACAAATCTCAGAGTGCTCTCATGAAGCAGGTGGAGGAGTTGAT
-----+-----+-----+-----+-----+-----+ 5040
CCTATAGTCATTTCATGCTGTTTAGAGTCTCACGAGAGTACTTCGTCCACCTCCTCAACTA
b D I S K Y D K S Q S A L M K Q V E E L I -

5041 ACTCTTGACACTTGGTGTGATAGAGAAGTTTTGTCTACTTTCTTTTGTGGTGAGTATGA
-----+-----+-----+-----+-----+-----+ 5100
TGAGAACTGTGAACCACAACCTATCTCTTCAAACAGATGAAAGAAAACACCACTCATACT
b L L T L G V D R E V L S T F F C G E Y D -

5101 TAGCGTCGTGAGAACGATGACGAAGGAATTGGTGTGTCTGTCTGGCTCTCAGAGGCGCAG
-----+-----+-----+-----+-----+-----+ 5160
ATCGCAGCACTCTTGCTACTGCTTCCTTAACCACAACAGACAGCCGAGAGTCTCCGCGTC
b S V V R T M T K E L V L S V G S Q R R S -

5161 TGGTGGTGCTAACACGTGGTTGGGAAATAGTTTAGTCTTGTGCACCTTGTGTCCGTAGT
-----+-----+-----+-----+-----+-----+ 5220
ACCACCACGATTGTGCACCAACCTTTTATCAAATCAGAACACGTGGAACAACAGGCATCA
b G G A N T W L G N S L V L C T L L S V V -

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FIG. 18I

5221 ACTTAGGGGATTAGATTATAGTTATATTGTAGTTAGCGGTGATGATAGCCTTATATTTAG
-----+-----+-----+-----+-----+-----+ 5280
TGAATCCCCTAATCTAATATCAATATAACATCAATCGCCACTACTATCGGAATATAAATC
b L R G L D Y S Y I V V S G D D S L I F S -

5281 TCGGCAGCCGTTGGATATTGATACGTCGGTCTGAGCGATAATTTTGGTTTTGACGTAAA
-----+-----+-----+-----+-----+-----+ 5340
AGCCGTCGGCAACCTATAACTATGCAGCCAAGACTCGCTATTAAAACCAAACTGCATTT
b R Q P L D I D T S V L S D N F G F D V K -

5341 GATTTTAAACCAAGCTGCTCCATATTTTGTCTAAGTTTGTAGTTCAAGTCGAGGATAG
-----+-----+-----+-----+-----+-----+ 5400
CTAAAAATGGTTCGACGAGGTATAAAAACAAGATTCAAAAATCAAGTTCAGCTCCTATC
b I F N Q A A P Y F C S K F L V Q V E D S -

5401 TCTCTTTTGTTCCTCCGATCCACTTAACTCTTCGTTAAGTTTGGAGCTTCCAAAACCTTC
-----+-----+-----+-----+-----+-----+ 5460
AGAGAAAAACAAGGGCTAGGTGAATTTGAGAAGCAATTCAAACCTCGAAGGTTTGAAG
b L F F V P D P L K L F V K F G A S K T S -

5461 AGATATCGACCTTTTACATGAGATTTTCAATCTTTCGTCGATCTTTCGAAGGGTTTCAA
-----+-----+-----+-----+-----+-----+ 5520
TCTATAGCTGGAAAATGTACTCTAAAAAGTTAGAAAGCAGCTAGAAAGCTTCCCAAAGTT
b D I D L L H E I F Q S F V D L S K G F N -

5521 TAGAGAGGACGTCATCCAGGAATTAGCTAAGCTGGTGACGCGGAAATATAAGCATTCCGGG
-----+-----+-----+-----+-----+-----+ 5580
ATCTCTCCTGCAGTAGGTCTTAATCGATTTCGACCACTGCGCCTTTATATTTCGTAAGCCC
b R E D V I Q E L A K L V T R K Y K H S G -

5581 ATGGACCTACTCGGCTTTGTGTGTCTTGCACGTTTTAAGTGCAAATTTTTCGCAGTTCTG
-----+-----+-----+-----+-----+-----+ 5640
TACCTGGATGAGCCGAAACACACAGAACGTGCAAATTCACGTTTAAAAGCGTCAAGAC
b W T Y S A L C V L H V L S A N F S Q F C -

5641 TAGGTTATATTACCACAATAGCGTGAATCTCGATGTGCGCCCTATTCAGAGGACCGAGTC
-----+-----+-----+-----+-----+-----+ 5700
ATCCAATATAATGGTGTATCGCACTTAGAGCTACACGCGGGATAAGTCTCCTGGCTCAG
b R L Y Y H N S V N L D V R P I Q R T E S -

5701 GCTTTCCTTGCTGGCCTTGAAGGCAAGAATTTTAAGGTGAAAGCTTCTCGTTTTGCCTT
-----+-----+-----+-----+-----+-----+ 5760
CGAAAGGAACGACCGGAACCTTCCGTTCTTAAATTCACCTTTCGAAGAGCAAAACGGAA
b L S L L A L K A R I L R W K A S R F A F -

5761 TTCGATAAAGAGGGGTTAATCGCGTTGGCCACGCTATAGTGTTCGTGCTCGGTTCTT
-----+-----+-----+-----+-----+-----+ 5820
AAGCTATTTCTCCCAATTAGCGCAACCGGTGCGATATCACAAAGACACGGAGCCAAGAA
b S I K R G * -

5821 CGTGAGGTTAATACCGAAGGGTCGTCTACTTATCTCAGTTATTTATTTTTTCGTCTTCT
-----+-----+-----+-----+-----+-----+ 5880
GCACTCCAATTATGGCTTCCCAGCAGCATGAATAGAGTCAATAAATAAAAAGCAGAAGA

5881 CTTAGGCGTGCCATCCGTGAAGTTAATACCGGTGGCACTCCTTCTCGAAGTGGGTATTAA
-----+-----+-----+-----+-----+-----+ 5940
GAATCCGCACGGTAGGCACTTCAATTATGGCCACCGTGAGGAAGAGCTTCAACCATAATT

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FIG. 18J

AGACCAAATTTTTATTGTGTGTACTTTTTGTTTTGTTACACCGTGAGGACAAGACC
5941 -----+-----+-----+-----+-----+-----+ 6000
TCTGGTTTTAAAAATAAACACACATGAAAAACAAAACAAGTGTGGCACTCCTGTTCTGG

ORF2 (7K)

GGTGAACATGTACAGTAGAGGGTCTTTCTTTAAGTCTCGGGTTACCCTTCTACTCTTG
6001 -----+-----+-----+-----+-----+-----+ 6060
CCACCTTGATACATGTCATCTCCAGAAAGAAATTCAGAGCCCAATGGGAAGGATGAGAAC
M Y S R G S F F K S R V T L P T L V -

TCGGAGCATAACATGTGGGAGTTTGAACCTCCCGTATCTTACGGACAAGAGACACATCAGCT
6061 -----+-----+-----+-----+-----+-----+ 6120
AGCCTCGTATGTACACCCTCAAACCTTGAGGGCATAGAATGCCTGTTCTCTGTGTAGTCTGA
G A Y M W E F E L P Y L T D K R H I S Y -

ATAGCGCGCCAAGTGTGCGGACTTTTAGCCTTGTGTGCGAGGTAGGATAGGGGCCAACAGG
6121 -----+-----+-----+-----+-----+-----+ 6180
TATCGCGCGGTTTACAGCGCTGAAATCGGAACACAGCTCCATCCTATCCCCGGTTGTCC
S A P S V A T F S L V S R *

TGACCAACAGCCTGCACCTAAGGTGCGCTGGAAGTGTGGATTGCTCAGTGTGCCAA
6181 -----+-----+-----+-----+-----+-----+ 6240
ACTGGTTGTGCGACGTGAATTCCACGCGACCTTCACAACCTAAACCAGAGTCACACGGTT

ATATCCTTTTAGGCGATGTACAGGAGTCTAGTTTAGTGTGTCTTTGGGGGATGACGGGAG
6241 -----+-----+-----+-----+-----+-----+ 6300
TATAGGAAAATCCGCTACATGTCTCAGATCAAATCACACAGAAACCCCTACTGCCCTC

CGACTAGGTTTAGGACTGTAGCTGCTATGTAAGTCGTGCATGCGGCATTGTGCGTAAGAC
6301 -----+-----+-----+-----+-----+-----+ 6360
GCTGATCCAAATCCTGACATCGACGATACATTACGACGTACGCCGTAACACGCATTCTG

GTGCATGCATTTGGGCGAGTGCCCTAGGGCAGCGTCGGTCAGGTGACTAGCAGCCGGGCTC
6361 -----+-----+-----+-----+-----+-----+ 6420
CACGTACGTAAACCCGCTCACGGGATCCCGTCGCAGCCAGTCCACTGATCGTCGGCCGAG

TACGGAGCGCTGAAAGTGCTAGGTCCTGAAGGTACAGTTGGGCTGAGGCAGGACATGGTT
6421 -----+-----+-----+-----+-----+-----+ 6480
ATGCCTCGCGACTTTCAGATCCAGGACTTCCATGTCAACCCGACTCCGTCTGTACCAA

GAACGAGTTGACCGTGGGGACCAGCGGCGGTGACTCGGGCCGTAGCCACGCGCGGGGCGG
6481 -----+-----+-----+-----+-----+-----+ 6540
CTTGCTCAACTGGCACCCCTGGTCGCCGCCACTGAGCCCGGCATCGGTGCGCGCCCCGCC

CAGGGCGTCTCGTGGTGTATCTGGGCAAGATACGGCTTTATTAGGCACCATAATATGGAG
6541 -----+-----+-----+-----+-----+-----+ 6600
GTCCCGCAGAGCACCACATAGACCGTTCTATGCCGAAATAATCCGTGGTATTATACCTC

CCCAAAGCGTCGGGGTCGGGAAACATCTCCATAGCTTAGTGGCAGCAGCCTAAGATAGGC
6601 -----+-----+-----+-----+-----+-----+ 6660
GGGTTTCGCAGCCCCAGCCCTTTGTAGAGGTATCGAATCACCGTCGTCCGATTCTATCCG

TGGGAGGCCCGTTCCCTGTAGTAGTGGTGGGTTAGCATGCCACTAAGCGGTGCGGCGTGA
6661 -----+-----+-----+-----+-----+-----+ 6720
ACCCTCCGGGCAAGGGACATCATCACCAACCAATCGTACGGTGATTCGCCACGCCGCACT

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FIG. 18K

TAAGGCGCCACCGTCCGTAGTTAGGCGACCCGTGTTTTAATAGGGTCTCTTTAGTTAAGT
6721 -----+-----+-----+-----+-----+-----+ 6780
ATTCCGCGGTGGCAGGCATCAATCCGCTGGGCACAAAATTATCCAGAGAAATCAATTCA

TTAGGCATGTCGTACAGTTAGGATTTCTTTTTAGATATTCTTTTATTTTTATTGTTTGT
6781 -----+-----+-----+-----+-----+-----+ 6840
AATCCGTACAGCATGTCAATCCTAAAGAAAAATCTATAAGAAAAATAAAAAATAACAAACA

TAGTTTAGATGTACATTATTACGTAGGTTACTTTGGCGCTACGCCAGAGGTTTTTCCTCT
6841 -----+-----+-----+-----+-----+-----+ 6900
ATCAAATCTACATGTAATAATGCATCCAATGAAACCGCGATGCGGTCTCCAAAAGGAGA

TTGTGTGTAGCCTTTAATGTAGGTTTCTTTGTTTTATTTTTGCCTTTCAGGCGGCGCGTT
6901 -----+-----+-----+-----+-----+-----+ 6960
AACACACATCGGAAATTACATCCAAAGAAACAAAATAAAAACGGAAAGTCCGCCGCGCAA

TCTTTTCTTCTATTTAGGTTTATCTTCTTTCTTTAGTGTTGTCGTATATGACGCTACGTC
6961 -----+-----+-----+-----+-----+-----+ 7020
AGAAAAGAAGATAAATCCAAATAGAAGAAAGGAATCACACAGCATATACTGCGATGCAG

CAAATTATGAATTTTCTTTCGTGTAGGCGTCGTTGAGTGCGTTCATCGGCGCTAGACGAG
7021 -----+-----+-----+-----+-----+-----+ 7080
GTTTAATACTTAAAAGGAAGCACATCCGCAGCAACTCACGCAAGTAGCCGCGATCTGCTC

GTTTAGTGGCGACATAAATAGGTTTTTGCGCGAGATTGGGATAGAACGAGTTTCGCCTTAA
7081 -----+-----+-----+-----+-----+-----+ 7140
CAAATCACCGCTGTATTTATCCAAAACGCGCTCTAACCCTATCTTGCTCAAGCGGAATT

AAGAGAAATCGGGGAAGGCGCCACGCGAATGACCTTCGTGCTGAGCGAAGGTAGTATCGT
7141 -----+-----+-----+-----+-----+-----+ 7200
TTCTCTTTAGCCCCCTCCGCGGTGCGCTTACTGGAAGCACGACTCGCTTCCATCATAGCA

ORF3 (5K, Membrane protein)

GATTTTATATTGAAGTAGGCGTATTTGTTTATGGATGATTTTAAACAGGCAATACTGTTG
7201 -----+-----+-----+-----+-----+-----+ 7260
CTAAAATATAACTTCATCCGCATAAAACAAATACCTACTAAAATTTGTCCGTTATGACAAC
a M D D F K Q A I L L -

CTAGTAGTCGATTTTGTCTTCGTGATAATTCTGCTGCTGGTTCTTACGTTTCGTGCTCCCG
7261 -----+-----+-----+-----+-----+-----+ 7320
GATCATCAGCTAAAACAGAAGCACTATTAAGACGACGACCAAGAATGCAAGCAGCAGGGC
a L V V D F V F V I I L L L V L T F V V P -

AGGTTACAGCAAAGCTCCACCATTAAATACAGGTCTTAGGACAGTGTGATTCTCCTTTAG
7321 -----+-----+-----+-----+-----+-----+ 7380
TCCAATGTCGTTTCGAGGTGGTAATTATGTCCAGAATCCTGTACACTAAGGAGGAAATC
a R L Q Q S S T I N T G L R T V * -

ORF4 (HSP70 Homolog)

TTAGATATGGAAGTAGGTATAGATTTTGAACCACTTTCAGCACAATCTGCTTTTCCCCA
7381 -----+-----+-----+-----+-----+-----+ 7440
AATCTATACCTTCATCCATATCTAAAACCTTGGTGAAAGTCGTGTTAGACGAAAAGGGGT
a M E V G I D F G T T F S T I C F S P -

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FIG. 18L

7441 TCTGGGGTCAGCGGTTGTACTCCTGTGGCCGGTAGTGTTTACGTTGAAACCCAAATTTT
+-----+-----+-----+-----+-----+-----+ 7500
AGACCCAGTCGCCAACATGAGGACACCGCCATCACAAATGCAACTTTGGGTTTAAAAA
a S G V S G C T P V A G S V Y V E T Q I F -

7501 ATACCTGAAGGTAGCAGTACTTACTTAATTGGTAAAGCTGCGGGGAAAGCTTATCGTGAC
+-----+-----+-----+-----+-----+-----+ 7560
TATGGACTTCCATCGTCATGAATGAATTAACCATTTTCGACGCCCTTTTGAATAGCACTG
a I P E G S S T Y L I G K A A G K A Y R D -

7561 GGTGTAGAGGGAAGGTTGTATGTTAACCCGAAAAGGTGGGCAGGTGTGACGAGGGATAAC
+-----+-----+-----+-----+-----+-----+ 7620
CCACATCTCCCTTCCAACATACAATTGGGCTTTTCCACCCGTCCACACTGCTCCCTATTG
a G V E G R L Y V N P K R W A G V T R D N -

7621 GTCGAACGCTACGTCGAGAAATTAAAACCTACATACACCGTGAAGATAGACAGCGGAGGC
+-----+-----+-----+-----+-----+-----+ 7680
CAGCTTGCATGACGCTCTTTAATTTTGGATGTATGTGGCACTTCTATCTGTGCCTCCG
a V E R Y V E K L K P T Y T V K I D S G G -

7681 GCCTTATTAATTGGAGGTTTAGGTTCCGGACCAGACACCTTATTGAGGGTCGTTGACGTA
+-----+-----+-----+-----+-----+-----+ 7740
CGGAATAATTAACCTCCAAATCCAAGGCCTGGTCTGTGGAATACTCCCAGCAACTGCAT
a A L L I G G L G S G P D T L L R V V D V -

7741 ATATGTTTATTCTTGAGAGCCTTGATACTGGAGTCCGAAAGGTATACGTCTACGACGGTT
+-----+-----+-----+-----+-----+-----+ 7800
TATACAAATAAGAACTCTCGGAATATGACCTCACGCTTTCCATATGCAGATGCTGCCAA
a I C L F L R A L I L E C E R Y T S T T V -

7801 ACAGCAGCTGTTGTAACGGTACCGGCTGACTATAACTCCTTTAAACGAAGCTTCGTTGTT
+-----+-----+-----+-----+-----+-----+ 7860
TGTCGTCGACAACATTGCCATGGCCGACTGATATTGAGGAAATTTGCTTCGAAGCAACAA
a T A A V V T V P A D Y N S F K R S F V V -

7861 GAGGCGCTAAAAGGTCTTGGTATACCGGTTAGAGGTGTTGTTAACGAACCGACGGCCGCA
+-----+-----+-----+-----+-----+-----+ 7920
CTCCGCGATTTTCCAGAACCATATGGCCAATCTCCACAACAATTGCTTGGCTGCCGGCGT
a E A L K G L G I P V R G V V N E P T A A -

7921 GCCCTCTATTCCTTAGCTAAGTCGCGAGTAGAAGACCTATTATTAGCGGTTTTTGATTTT
+-----+-----+-----+-----+-----+-----+ 7980
CGGGAGATAAGGAATCGATTGACGCTCATCTTCTGGATAATAATCGCCAAAACTAAAA
a A L Y S L A K S R V E D L L L A V F D F -

7981 GGGGAGGGACTTTTCGACGTCTCATTCGTTAAGAAGAAGGGAAATATACTATGCGTCATC
+-----+-----+-----+-----+-----+-----+ 8040
CCCCCTCCCTGAAAGCTGCAGAGTAAGCAATTCTTCTCCCTTTATATGATACGCAGTAG
a G G G T F D V S F V K K K G N I L C V I -

8041 TTTTCAGTGGGTGATAATTTCTTGGGTGGTAGAGATATTGATAGAGCTATCGTGGAAGTT
+-----+-----+-----+-----+-----+-----+ 8100
AAAAGTCACCCACTATTAAAGAACCCACCATCTCTATAACTATCTCGATAGCACCTTCAA
a F S V G D N F L G G R D I D R A I V E V -

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FIG. 18M

8101 ATCAAACAAAAGATCAAAGGAAAGGCGTCTGATGCCAAGTTAGGGATATTCGTATCCTCG
-----+-----+-----+-----+-----+ 8160
TAGTTTGTTCCTTTCTAGTTTCCTTTCCGCAGACTACGGTTCAATCCCTATAAGCATAGGAGC
a I K Q K I K G K A S D A K L G I F V S S -

8161 ATGAAGGAAGACTTGTCTAACAATAACGCTATAACGCAACACCTTATCCCCGTAGAAGGG
-----+-----+-----+-----+-----+ 8220
TACTTCCTTCTGAACAGATTGTTATTGCGATATTGCGTTGTGGAATAGGGGCATCTTCCC
a M K E D L S N N N A I T Q H L I P V E G -

8221 GGTGTGGAGGTTGTGGATTTGACTAGCGACGAACTGGACGCAATCGTTGCACCATTCAGC
-----+-----+-----+-----+-----+ 8280
CCACACCTCCAACACCTAAACTGATCGCTGCTTGACCTGCGTTAGCAACGTGGTAAGTCG
a G V E V V D L T S D E L D A I V A P F S -

8281 GCTAGGGCTGTGGAAGTATTCAAACTGGTCTTGACAACCTTTTACCCAGACCCGGTTATT
-----+-----+-----+-----+-----+ 8340
CGATCCCAGACCTTCATAAGTTTGTGACCAGAACTGTTGAAAATGGGTCTGGGCCAATAA
a A R A V E V F K T G L D N F Y P D P V I -

8341 GCCGTTATGACTGGGGGGTCAAGTGCTCTAGTTAAGGTCAGGAGTGATGTGGCTAATTTG
-----+-----+-----+-----+-----+ 8400
CGGCAATACTGACCCCCAGTTCACGAGATCAATTCAGTCCTCACTACACCGATTAAAC
a A V M T G G S S A L V K V R S D V A N L -

8401 CCGCAGATATCTAAAGTCGTGTTTCGACAGTACCGATTTTAGATGTTCCGTGGCTTGTGGG
-----+-----+-----+-----+-----+ 8460
GGCGTCTATAGATTTTACGACAAAGCTGTCTATGGCTAAAATCTACAAGCCACCGAACCCC
a P Q I S K V V F D S T D F R C S V A C G -

8461 GCTAAGGTTTACTGCGATACTTTGGCAGGTAATAGCGGACTGAGACTGGTGGACACTTTA
-----+-----+-----+-----+-----+ 8520
CGATTCCAAATGACGCTATGAAACCGTCCATTATCGCCTGACTCTGACCACCTGTGAAAT
a A K V Y C D T L A G N S G L R L V D T L -

8521 ACGAATACGCTAACGGACGAGGTAGTGGGTCTTCAGCCGGTGGTAATTTTCCCGAAAGGT
-----+-----+-----+-----+-----+ 8580
TGCTTATGCGATTGCCTGCTCCATCACCAGAAAGTCCGCCACCATTAAGGGCTTTCCA
a T N T L T D E V V G L Q P V V I F P K G -

8581 AGTCCAATACCCTGTTTCATATACTCATAGATACACAGTGGGTGGTGGAGATGTGGTATAC
-----+-----+-----+-----+-----+ 8640
TCAGGTTATGGGACAAGTATATGAGTATCTATGTGTCACCCACCACCTCTACACCATATG
a S P I P C S Y T H R Y T V G G G D V V Y -

8641 GGTATATTTGAAGGGGAGAATAACAGAGCTTTTCTAAATGAGCCGACGTTCCGGGGCGTA
-----+-----+-----+-----+-----+ 8700
CCATATAAACTTCCCCTCTTATTGTCTCGAAAAGATTTACTCGGCTGCAAGGCCCCGCAT
a G I F E G E N N R A F L N E P T F R G V -

8701 TCGAAACGTAGGGGAGACCCAGTAGAGACCGACGTGGCGCAGTTTAATCTCTCCACGGAC
-----+-----+-----+-----+-----+ 8760
AGCTTTGCATCCCCCTCTGGGTCTCTGCTGACCCGCGTCAAATTAGAGAGGTGCCTG
a S K R R G D P V E T D V A Q F N L S T D -

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FIG. 18N

8761 GGAACGGTGTCTGTTATCGTTAATGGTGAGGAAGTAAAGAATGAATATCTGGTACCCGGG 8820
-----+-----+-----+-----+-----+-----+
CCTTGCCACAGACAATAGCAATTACCACTCCTTCATTTCTTACTTATAGACCATGGGCCC
a G T V S V I V N G E E V K N E Y L V P G -

8821 ACAACAAACGTACTGGATTTCATTGGTCTATAAATCTGGGAGAGAAGATTTAGAGGCTAAG 8880
-----+-----+-----+-----+-----+-----+
TGTTGTTTGCATGACCTAAGTAACCAGATATTTAGACCCTCTCTTCTAAATCTCCGATTCT
a T T N V L D S L V Y K S G R E D L E A K -

8881 GCAATACCAGAGTACTTGACCACACTGAATATTTTGCACGATAAGGCTTTTCACGAGGAGA 8940
-----+-----+-----+-----+-----+-----+
CGTTATGGTCTCATGAACTGGTGTGACTTATAAAACGTGCTATTCCGAAAGTGCTCCTCT
a A I P E Y L T T L N I L H D K A F T R R -

8941 AACCTGGGTAACAAAGATAAGGGGTTCTCGGATTTAAGGATAGAAGAAAATTTTAAAA 9000
-----+-----+-----+-----+-----+-----+
TTGGACCCATTGTTTCTATTCCCCAAGAGCCTAAATTCCTATCTTCTTTTAAAAAATTTT
a N L G N K D K G F S D L R I E E N F L K -

ORF5 (HSP90 Homolog)

9001 TCCGCCGTAGATACAGACACGATTTTGAATGGATAAATATATTTATGTAACGGGGATATT 9060
-----+-----+-----+-----+-----+-----+
AGGCGGCATCTATGTCTGTGCTAAAACTTACCTATTTATATAAATACATTGCCCTATAA
a S A V D T D T I L N G *
b M D K Y I Y V T G I L -

9061 AAACCCTAACGAGGCTAGAGACGAGGTATTCTCGGTAGTGAATAAGGGATATATTGGACC 9120
-----+-----+-----+-----+-----+-----+
TTTGGGATTGCTCCGATCTCTGCTCCATAAGAGCCATCACTTATCCCTATATAACCTGG
b N P N E A R D E V F S V V N K G Y I G P -

9121 GGGAGGGCGCTCCTTTTTCGAATCGTGGTAGTAAGTACACCGTCGTCTGGGAAACTCTGC 9180
-----+-----+-----+-----+-----+-----+
CCCTCCCGCGAGGAAAAGCTTAGCACCATCATTCATGTGGCAGCAGACCCTTTTGAGACG
b G G R S F S N R G S K Y T V V W E N S A -

9181 TGCGAGGATTAGTGGATTTACGTCGACTTCGCAATCTACGATAGATGCTTTTCGCGTATTT 9240
-----+-----+-----+-----+-----+-----+
ACGCTCCTAATCACCTAAATGCAGCTGAAGCGTTAGATGCTATCTACGAAAGCGCATAAA
b A R I S G F T S T S Q S T I D A F A Y F -

9241 CTTGTTGAAAGGCGGATTGACTACCACGCTCTCTAACCCAATAAACTGTGAGAATTGGGT 9300
-----+-----+-----+-----+-----+-----+
GAACAACCTTCCGCCTAACTGATGGTGCAGAGATTGGGTATTTGACACTCTTAACCCA
b L L K G G L T T T L S N P I N C E N W V -

9301 CAGGTCATCTAAGGATTTAAGCGCGTTTTTTCAGGACCCTAATTAAAGGTAAGATTTATGC 9360
-----+-----+-----+-----+-----+-----+
GTCCAGTAGATTCTAAATTCGCGCAAAAAGTCCTGGGATTAATTTCCATTCTAAATACG
b R S S K D L S A F F R T L I K G K I Y A -

9361 ATCGCGTTCTGTGGACAGCAATCTTCCAAAGAAAGACAGGGATGACATCATGGAAGCGAG 9420
-----+-----+-----+-----+-----+-----+
TAGCGCAAGACACCTGTCGTTAGAAGGTTTCTTTCTGTCCCTACTGTAGTACCTTCGCTC
b S R S V D S N L P K K D R D D I M E A S -

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FIG. 180

TCGACGACTATCGCCATCGGACGCCGCCCTTTTGCAGAGCAGTGTCCGGTTCAGGTAGGGAA
9421 -----+-----+-----+-----+-----+-----+ 9480
AGCTGCTGATAGCGGTAGCCTGCGGCGGAAAACGTCTCGTCACAGCCAAGTCCATCCCTT
b R R L S P S D A A F C R A V S V Q V G K -

GTATGTGGACGTAACGCAGAATTTAGAAAGTACGATCGTGCCGTTAAGAGTTATGGAAAT
9481 -----+-----+-----+-----+-----+-----+ 9540
CATAACCTGCATTGCGTCTTAAATCTTTTCATGCTAGCACGGCAATTCTCAATACCTTTA
b Y V D V T Q N L E S T I V P L R V M E I -

AAAGAAAAGACGAGGATCAGCACATGTTAGTTTACCGAAGGTGGTATCCGCTTACGTAGA
9541 -----+-----+-----+-----+-----+-----+ 9600
TTTCTTTTCTGCTCCTAGTCGTGTACAATCAAATGGCTTCCACCATAGGCGAATGCATCT
b K K R R G S A H V S L P K V V S A Y V D -

TTTTTATACGAACTTGCAGGAATTGCTGTCCGATGAAGTAACTAGGGCCAGAACCGATAC
9601 -----+-----+-----+-----+-----+-----+ 9660
AAAAATATGCTTGAACGTCCTTAACGACAGCCTACTTCATTGATCCCGGTCTTGGCTATG
b F Y T N L Q E L L S D E V T R A R T D T -

AGTTTCGGCATACTACCGACTCTATGGCTTTCTTAGTTAAGATGTTACCCCTGACTGC
9661 -----+-----+-----+-----+-----+-----+ 9720
TCAAAGCCGTATGCGATGGCTGAGATACCGAAAGAATCAATTCTACAATGGGGACTGACG
b V S A Y A T D S M A F L V K M L P L T A -

TCGTGAGCAGTGGTTAAAAGACGTGCTAGGATATCTGCTGGTACGGAGACGACCAGCAAA
9721 -----+-----+-----+-----+-----+-----+ 9780
AGCACTCGTCACCAATTTTCTGCACGATCCTATAGACGACCATGCCTCTGCTGGTCTGTTT
b R E Q W L K D V L G Y L L V R R R P A N -

TTTTTCCTACGACGTAAGAGTAGCTTGGGTATATGACGTGATCGCTACGCTCAAGCTGGT
9781 -----+-----+-----+-----+-----+-----+ 9840
AAAAAGGATGCTGCATTCTCATCGAACCCATATACTGCACTAGCGATGCGAGTTCCGACCA
b F S Y D V R V A W V Y D V I A T L K L V -

CATAAGATTGTTTTTCAACAAGGACACACCCGGGGGTATTAAAGACTTAAAACCGTGTGT
9841 -----+-----+-----+-----+-----+-----+ 9900
GTATTCTAACAAGAGTTGTTTCTGTGTGGGCCCCCATAATTTCTGAATTTGGCACACA
b I R L F F N K D T P G G I K D L K P C V -

GCCTATAGAGTCATTCGACCCCTTTCACGAGCTTTTCGTCCTATTTCTCTAGGTTAAGTTA
9901 -----+-----+-----+-----+-----+-----+ 9960
CGGATATCTCAGTAAGCTGGGGAAAGTGCTCGAAAGCAGGATAAAGAGATCCAATTCAT
b P I E S F D P F H E L S S Y F S R L S Y -

CGAGATGACGACAGGTAAAGGGGAAAGATATGCCCCGAGATCGCCGAGAAGTTGGTGCG
9961 -----+-----+-----+-----+-----+-----+ 10020
GCTCTACTGCTGTCCATTTCCCCCTTTCTATACGGGCTCTAGCGGCTCTTCAACCACGC
b E M T T G K G G K I C P E I A E K L V R -

CCGTCTAATGGAGGAAAACCTATAAGTTAAGATTGACCCCAAGTGATGGCCTTAATAATTAT
10021 -----+-----+-----+-----+-----+-----+ 10080
GGCAGATTACCTCCTTTTGATATTCAATTCTAACTGGGGTCACTACCGGAATTATTAATA
b R L M E E N Y K L R L T P V M A L I I I -

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FIG. 18P

10081 ACTGGTATACTACTCCATTTACGGCACAAACGCTACCAGGATTAAAAGACGCCCCGGATTT
-----+-----+-----+-----+-----+-----+ 10140
TGACCATATGATGAGGTAAATGCCGTGTTTGCATGGTCCTAATTTTCTGCGGGCCTAAA
b L V Y Y S I Y G T N A T R I K R R P D F -

10141 CCTCAATGTGAGGATAAAGGGAAGAGTCGAGAAGGTTTCGTTACGGGGGGTAGAAGATCG
-----+-----+-----+-----+-----+-----+ 10200
GGAGTTACACTCCTATTTCCCTTCTCAGCTCTTCCAAAGCAATGCCCCCATCTTCTAGC
b L N V R I K G R V E K V S L R G V E D R -

10201 TGCCTTTAGAATATCAGAAAAGCGCGGGATAAACGCTCAACGTGTATTATGTAGGTACTA
-----+-----+-----+-----+-----+-----+ 10260
ACGGAAATCTTATAGTCTTTTCGCGCCCTATTTGCGAGTTGCACATAATACATCCATGAT
b A F R I S E K R G I N A Q R V L C R Y Y -

10261 TAGCGATCTCACATGTCTGGCTAGGCGACATTACGGCATTTCGAGGAACAATTGGAAGAC
-----+-----+-----+-----+-----+-----+ 10320
ATCGCTAGAGTGACAGACCGATCCGCTGTAATGCCGTAAGCGTCCTTGTAAACCTTCTG
b S D L T C L A R R H Y G I R R N N W K T -

10321 GCTGAGTTATGTAGACGGGACGTTAGCGTATGACACGGCTGATTGTATAACTTCTAAGGT
-----+-----+-----+-----+-----+-----+ 10380
CGACTCAATACATCTGCCCTGCAATCGCATACTGTCCGACTAACATATTGAAGATTCCA
b L S Y V D G T L A Y D T A D C I T S K V -

10381 GAGAAATACGATCAACACCGCAGATCACGCTAGCATTATACACTATATCAAGACGAACGA
-----+-----+-----+-----+-----+-----+ 10440
CTCTTTATGCTAGTTGTGGCGTCTAGTGCGATCGTAATATGTGATATAGTTCTGCTTGCT
b R N T I N T A D H A S I I H Y I K T N E -

10441 AAACCAGGTTACCGGAACTACTCTACCACACCAGCTTTAAAGCTGCGTGTAGTATGCGAC
-----+-----+-----+-----+-----+-----+ 10500
TTTGGTCCAATGGCCTTGATGAGATGGTGTGGTCGAAATTTTCGACGCACATCATACGCTG
b N Q V T G T T L P H Q L * -

10501 GATGTTTCTCGTATTAGTTTTATAAAAATTTTTAATTGCTCTGTGTGTGGTTTTTGTGTA
-----+-----+-----+-----+-----+-----+ 10560
CTACAAAGAGCATAATCAAAATATTTTTAAAAATTAACGAGACACACACCAAAAACAAC

ORF6 (Coat protein)

10561 GTGAACGCGATGGCATTGAACTGAAATTAGGGCAGATATATGAAGTCGTCCCCGAAAT
-----+-----+-----+-----+-----+-----+ 10620
CACTTGCGCTACCGTAAACTTGACTTTAATCCCGTCTATATACTTCAGCAGGGGCTTTTA
a M A F E L K L G Q I Y E V V P E N -

10621 AATTTGAGAGTTAGAGTGGGGGATGCGGCACAAGGAAAATTTAGTAAGGCGAGTTTCTTA
-----+-----+-----+-----+-----+-----+ 10680
TTAAACTCTCAATCTCACCCCTACGCCGTGTTCCCTTTTAAATCATTCGCGCTCAAAGAAT
a N L R V R V G D A A Q G K F S K A S F L -

10681 AAGTACGTTAAGGACGGGACACAGCGGAATTAACGGGAATCGCCGTAGTCCCCGAAAAA
-----+-----+-----+-----+-----+-----+ 10740
TTCATGCAATTCCCTGCCCTGTGTCCGCCTTAATTGCCCTTAGCGGCATCACGGGCTTTTT
a K Y V K D G T Q A E L T G I A V V P E K -

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FIG. 18Q

10741 TACGTATTTCGCCACAGCAGCTTTGGCTACAGCGGCGCAGGAGCCACCTAGGCAGCCACCA 10800
-----+-----+-----+-----+-----+-----+
a ATGCATAAGCGGTGTCGTCGAAACCGATGTCGCCGCGTCCTCGGTGGATCCGTCGGTGGT
Y V F A T A A L A T A A Q E P P R Q P P -

10801 GCGCAAGTGGCGGAACCACAGGAAACCGATATAGGGGTAGTGCCGGAATCTGAGACTCTC 10860
-----+-----+-----+-----+-----+-----+
a CGCGTTACCGCCTTGGTGTCTTTGGCTATATCCCCATCACGGCCTTAGACTCTGAGAG
A Q V A E P Q E T D I G V V P E S E T L -

10861 ACACCAAATAAGTTGGTTTTTCGAGAAAGATCCAGACAAGTTCTTGAAGACTATGGGCAAG 10920
-----+-----+-----+-----+-----+-----+
a TGTGGTTTATTCAACCAAAGCTCTTTCTAGGTCTGTTCAAGAACTTCTGATACCCGTTT
T P N K L V F E K D P D K F L K T M G K -

10921 GGAATAGCTTTGGACTTGGCGGGAGTTACCCACAAACCGAAAGTTATTAACGAGCCAGGG 10980
-----+-----+-----+-----+-----+-----+
a CCTTATCGAAACCTGAACCGCCCTCAATGGGTGTTTGGCTTTCAATAATTGCTCGGTCCC
G I A L D L A G V T H K P K V I N E P G -

10981 AAAGTATCAGTAGAGGTGGCAATGAAGATTAATGCCGCATTGATGGAGCTGTGTAAGAAG 11040
-----+-----+-----+-----+-----+-----+
a TTTCATAGTCATCTCCACCGTTACTTCTAATTACGGCGTAACTACCTCGACACATTCTTC
K V S V E V A M K I N A A L M E L C K K -

11041 GTTATGGGCGCCGATGACGCAGCAACTAAGACAGAATTCTTCTTGTACGTGATGCAGATT 11100
-----+-----+-----+-----+-----+-----+
a CAATACCCGCGGCTACTGCGTCGTTGATTCTGTCTTAAGAAGAACATGCACTACGTCTAA
V M G A D D A A T K T E F F L Y V M Q I -

11101 GCTTGCACGTTCTTTACATCGTCTTCGACGGAGTTCAAAGAGTTTGA CTACATAGAAACC 11160
-----+-----+-----+-----+-----+-----+
a CGAACGTGCAAGAAATGTAGCAGAAGCTGCCTCAAGTTTCTCAAAC TGATGTATCTTTGG
A C T F F T S S S T E F K E F D Y I E T -

11161 GATGATGGAAAGAAGATATATGCGGTGTGGGTATATGATTGCATTAAACAAGCTGCTGCT 11220
-----+-----+-----+-----+-----+-----+
a CTACTACCTTTCTTCTATATACGCCACACCCATATACTAACGTAATTTGTTGACGACGA
D D G K K I Y A V W V Y D C I K Q A A A -

11221 TCGACGGGTTATGAAAACCCGGTAAGGCAGTATCTAGCGTACTTCACACCAACCTTCATC 11280
-----+-----+-----+-----+-----+-----+
a AGCTGCCCAATACTTTTGGGCCATTCCGTCATAGATCGCATGAAGTGTGGTTGGAAGTAG
S T G Y E N P V R Q Y L A Y F T P T F I -

11281 ACGGCGACCCTGAATGGTAAACTAGTGATGAACGAGAAGGTTATGGCACAGCATGGAGTA 11340
-----+-----+-----+-----+-----+-----+
a TGCCGCTGGGACTTACCATTTGATCACTACTTGCTCTTCCAATACCGTGTCTGACCTCAT
T A T L N G K L V M N E K V M A Q H G V -

11341 CCACCGAAATTCTTTCCGTACACGATAGACTGCGTTTCGTCCGACGTACGATCTGTTCAAC 11400
-----+-----+-----+-----+-----+-----+
a GGTGGCTTTAAGAAAGGCATGTGCTATCTGACGCAAGCAGGCTGCATGCTAGACAAGTTG
P P K F F P Y T I D C V R P T Y D L F N -

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FIG. 18R

11401 AACGACGCAATATTAGCATGGAATTTAGCTAGACAGCAGGCGTTTAGAAACAAGACGGTA
-----+-----+-----+-----+-----+ 11460
TTGCTGCGTTATAATCGTACCTTAAATCGATCTGTCTCCGCAAATCTTTGTTCTGCCAT
a N D A I L A W N L A R Q Q A F R N K T V -

11461 ACGGCCGATAACACCTTACACAACGTCTTCCAACCTATTGCAAAAGAAGTAGCTACGATCG
-----+-----+-----+-----+-----+ 11520
TGCCGGCTATTGTGGAATGTGTTGCAGAAGGTTGATAACGTTTTCTTCATCGATGCTAGC
a T A D N T L H N V F Q L L Q K K * -

11521 ATGTCTATAAATTGGTGAAAAATTTAGAAATATTTACCTTTTATTGATAATTCATGGGAG
-----+-----+-----+-----+-----+ 11580
TACAGATATTTAACCACCTTTTAAATCTTTATAAATGGAATAACTATTAAGTACCCCTC
a M S I N W * -
c M G A -

11581 CTTATACACATGTAGACTTTTCATGAGTCGCGGTTGCTGAAAGACAAACAAGACTATCTTT
-----+-----+-----+-----+-----+ 11640
GAATATGTGTACATCTGAAAGTACTCAGCGCCAACGACTTTCTGTTTGTCTGATAGAAA
c Y T H V D F H E S R L L K D K Q D Y L S -

11641 CTTTCAAGTCAGCGGATGAAGCTCCTCCTGATCCTCCCGGATACGTTTCGCCCAGATAGTT
-----+-----+-----+-----+-----+ 11700
GAAAGTTCAGTCGCCTACTTCGAGGAGGACTAGGAGGGCCTATGCAAGCGGGTCTATCAA
c F K S A D E A P P D P P G Y V R P D S Y -

11701 ATGTGAGGGCTTATTTGATACAAAGAGCAGACTTTCCCAATACTCAAAGCTTATCAGTTA
-----+-----+-----+-----+-----+ 11760
TACACTCCCGAATAAACTATGTTTCTCGTCTGAAAGGGTTATGAGTTTCAATAGTCAAT
c V R A Y L I Q R A D F P N T Q S L S V T -

11761 CGTTATCGATAGCCAGTAATAAGTTAGCTTCAGGTCTTATGGGAAGCGACGCAGTATCAT
-----+-----+-----+-----+-----+ 11820
GCAATAGCTATCGGTCATTATTCAATCGAAGTCCAGAATACCCCTTCGCTGCGTCATAGTA
c L S I A S N K L A S G L M G S D A V S S -

11821 CGTCGTTTATGCTGATGAACGACGTGGGAGATTACTTCGAGTGCGGCGTGTGTCAACA
-----+-----+-----+-----+-----+ 11880
GCAGCAAATACGACTACTTGCTGCACCCTCTAATGAAGCTCACGCCGCACACAGTGTTGT
c S F M-L-M-N-D-V G D Y F E C G V C H N K -

11881 AACCCTACTTAGGACGGGAAGTTATCTTCTGTAGGAAATACATAGGTGGGAGAGGAGTGG
-----+-----+-----+-----+-----+ 11940
TTGGGATGAATCCTGCCCTTCAATAGAAGACATCCTTTATGTATCCACCCTCTCCTCACC
c P Y L G R E V I F C R K Y I G G R G V E -

11941 AGATCACCCTGGTAAGAACTACACGTCGAACAATTGGAACGAGGCGTCGTACGTAATAC
-----+-----+-----+-----+-----+ 12000
TCTAGTGGTGACCATTCCTTGATGTGCAGCTTGTTAACCTTGCTCCGCAGCATGCATTATG
c I T T G K N Y T S N N W N E A S Y V I Q -

12001 AAGTGAACGTAGTCGATGGGTTAGCACAGACCACTGTTAATTCTACTTATACGCAAACGG
-----+-----+-----+-----+-----+ 12060
TTCACCTGCATCAGCTACCCAATCGTGTCTGGTGACAATTAAGATGAATATGCGTTTGCC
c V N V V D G L A Q T T V N S T Y T Q T D -

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FIG. 18S

12061 ACGTTAGTGGTCTACCCAAAAATTGGACGCGTATCTACAAAATAACAAAGATAGTGTCCG
-----+-----+-----+-----+-----+-----+ 12120
TGCAATCACCAGATGGGTTTTTAACCTGCGCATAGATGTTTTATTGTTTCTATCACAGGC
c V S G L P K N W T R I Y K I T K I V S V -

12121 TAGATCAGAACCTCTACCCTGGTTGTTTCTCAGACTCGAAACTGGGTGTAATGCGTATAA
-----+-----+-----+-----+-----+-----+ 12180
ATCTAGTCTTGGAGATGGGACCAACAAAGAGTCTGAGCTTTGACCCACATTACGCATATT
c D Q N L Y P G C F S D S K L G V M R I R -

12181 GGTCACGTGTTAGTTTCCCCAGTGCGCATCTTCTTTAGGGATATCTTATTGAAACCTTTGA
-----+-----+-----+-----+-----+-----+ 12240
-CCAGTGACAATCAAAGGGGTACGCGTAGAAGAAATCCCTATAGAATAACTTTGGAAACT
c S L L V S P V R I F F R D I L L K P L K -

12241 AGAAATCGTTCAACGCAAGAATCGAGGATGTGCTGAATATTGACGACACGTCGTTGTTAG
-----+-----+-----+-----+-----+-----+ 12300
TCTTTAGCAAGTTGCGTTCTTAGCTCCTACAGACTTATAACTGCTGTGCAGCAACAATC
c K S F N A R I E D V L N I D D T S L L V -

12301 TACCGAGTCCTGTGCTACCAGAGTCTACGGGAGGTGTAGGTCCATCAGAGCAGCTGGATG
-----+-----+-----+-----+-----+-----+ 12360
ATGGCTCAGGACAGCATGGTCTCAGATGCCCTCCACATCCAGGTAGTCTCGTCGACCTAC
c P S P V V P E S T G G V G P S E Q L D V -

12361 TAGTGGCTTTAACGTCCGACGTAACGGAATTGATCAACACTAGGGGGCAAGGTAAGATAT
-----+-----+-----+-----+-----+-----+ 12420
ATCACCAGAAATTGCAGGCTGCATTGCCTTAAGTAGTTGTGATCCCCGTTCCATTCTATA
c V A L T S D V T E L I N T R G Q G K I C -

12421 GTTTTCCAGACTCAGTGTATCGATCAATGAAGCGGATATCTACGATGAGCGGTATTTGC
-----+-----+-----+-----+-----+-----+ 12480
CAAAAGGTCTGAGTCACAATAGCTAGTTACTTCGCCTATAGATGCTACTCGCCATAAACG
c F P D S V L S I N E A D I Y D E R Y L P -

12481 CGATAACGGAAGCTCTACAGATAAACGCAAGACTACGCAGACTCGTTCTTTGAAAGGCG
-----+-----+-----+-----+-----+-----+ 12540
GCTATTGCCTTCGAGATGTCTATTTGCGTTCTGATGCGTCTGAGCAAGAAAGCTTTCCGC
c I T E A L Q I N A R L R R L V L S K G G -

12541 GGAGTCAAACACCACGAGATATGGGGAATATGATAGTGGCCATGATACAACCTTTTCGTAC
-----+-----+-----+-----+-----+-----+ 12600
CCTCAGTTTGTGGTGCTCTATACCCCTTATACTATCACCAGTACTATGTTGAAAAGCATG
c S Q T P R D M G N M I V A M I Q L F V L -

12601 TCTACTCTACTGTAAAGAATATAAGCGTCAAAGACGGGTATAGGGTGGAGACCGAATTAG
-----+-----+-----+-----+-----+-----+ 12660
AGATGAGATGACATTTCTTATATTTCGCAGTTTCTGCCCATATCCCACCTCTGGCTTAATC
c Y S T V K N I S V K D G Y R V E T E L G -

12661 GTCAAAGAGAGTCTACTTAAGTTATTCCGGAAGTAAGGGAAGCTATATTAGGAGGGAAAT
-----+-----+-----+-----+-----+-----+ 12720
CAGTTTTCTCTCAGATGAATTCAATAAGCCTTCATTCCCTTCGATATAATCCTCCCTTTA
c Q K R V Y L S Y S E V R E A I L G G K Y -

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FIG. 18T

12721 -----+-----+-----+-----+-----+-----+-----+ 12780
ACGGTGCGTCTCCAACCAACACTGTGCGATCCTTCATGAGGTATTTTGCTCACACCACTA
c TGCCACGCAGAGGTTGGTTGTGACACGCTAGGAAGTACTCCATAAAACGAGTGTGGTGAT
G A S P T N T V R S F M R Y F A H T T I -

12781 -----+-----+-----+-----+-----+-----+-----+ 12840
TTACTCTACTTATAGAGAAGAAAATTCAGCCAGCGTGTACTGCCCTAGCTAAGCACGGCG
c AATGAGATGAATATCTCTTCTTTTAAGTCGGTCGCACATGACGGGATCGATTTCGTGCCGC
T L L I E K K I Q P A C T A L A K H G V -

12841 -----+-----+-----+-----+-----+-----+-----+ 12900
TCCCGAAGAGGTTCACTCCGTACTGCTTCGACTTCGCACTACTGGATAACAGATATTACC
c AGGGCTTCTCCAAGTGAGGCATGACGAAGCTGAAGCGTGATGACCTATTGTCTATAATGG
P K R F T P Y C F D F A L L D N R Y Y P -

12901 -----+-----+-----+-----+-----+-----+-----+ 12960
CGGCGGACGTGTTGAAGGCTAACGCAATGGCTTGCGCTATAGCGATTAAATCAGCTAATT
c GCCGCCTGCACAACTTCCGATTGCGTTACCGAACCGGATATCGCTAATTTAGTCGATTAA
A D V L K A N A M A C A I A I K S A N L -

12961 -----+-----+-----+-----+-----+-----+-----+ 13020
TAAGGCGTAAAGGTTCCGAGACGTATAACATCTTAGAAAGCATTTGATTATCTAAAGATG
a ATTCCGCATTTCCAAGCCTCTGCATATTGTAGAATCTTTCGTAAACTAATAGATTTCTAC
c R R K G S E T Y N I L E S I * M -

13021 -----+-----+-----+-----+-----+-----+-----+ 13080
GAATTCAGACCAGTTTAAATTACAGTTCGCCGTGATCCCGGCGTAAACACTGGTAGTTTG
a CTTAAGTCTGGTCAAAATTAATGTCAAGCGGCACTAGGGCCGCATTTGTGACCATCAAAC
E F R P V L I T V R R D P G V N T G S L -

13081 -----+-----+-----+-----+-----+-----+-----+ 13140
AAAGTGATAGCTTATGACTTACACTACGACAATATATTCGATAACTGCGCGGTAAAGTCG
a TTTCACTATCGAATACTGAATGTGATGCTGTTATATAAGCTATTGACGCGCCATTTTCAGC
K V I A Y D L H Y D N I F D N C A V K S -

13141 -----+-----+-----+-----+-----+-----+-----+ 13200
TTTCGAGACACCGACACTGGATTCACTGTTATGAAAGAATACTCGACGAATTCAGCGTTC
a AAAGCTCTGTGGCTGTGACCTAAGTGACAATACTTTCTTATGAGCTGCTTAAGTCGCAAG
F R D T D T G F T V M K E Y S T N S A F -

13201 -----+-----+-----+-----+-----+-----+-----+ 13260
ATACTAAGTCCTTATAAACTGTTTCCGCGGTCTTTAATAAGGAAGGTGAGATGATAAGT
a TATGATTCAGGAATATTTGACAAAAGGCGCCAGAAATTATTCCTTCCACTCTACTATTCA
I L S P Y K L F S A V F N K E G E M I S -

13261 -----+-----+-----+-----+-----+-----+-----+ 13320
AACGATGTAGGATCGAGTTTCAGGGTTTACAATATCTTTTCGCAAATGTGTAAAGATATC
a TTGCTACATCCTAGCTCAAAGTCCCAAATGTTATAGAAAAGCGTTTACACATTTCTATAG
N D V G S S F R V Y N I F S Q M C K D I -

13321 -----+-----+-----+-----+-----+-----+-----+ 13380
AACGAGATCAGCGAGATACAACGCGCCGGTTACCTAGAAACATATTTAGGAGACGGGCAG
a TTGCTCTAGTCGCTCTATGTTGCGCGGCCAATGGATCTTTGTATAAATCCTCTGCCCGTC
N E I S E I Q R A G Y L E T Y L G D G Q -

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FIG. 18U

13381 GCTGACACTGATATATTTTTTGGATGTCTTAACCAACAACAAAGCAAAGGTAAGGTGGTTA
-----+-----+-----+-----+-----+-----+ 13440
CGACTGTGACTATATAAAAACTACAGAATTGGTTGTTGTTTCGTTTCCATTCCACCAAT
a A D T D I F F D V L T N N K A K V R W L -

13441 GTTAATAAAGACCATAGCGCGTGGTGTGGGATATTGAATGATTTGAAGTGGGAAGAGAGC
-----+-----+-----+-----+-----+-----+ 13500
CAATTATTTCTGGTATCGCGCACCACACCCTATAACTTACTAACTTCACCCTTCTCTCG
a V N K D H S A W C G I L N D L K W E E S -

13501 AACAAGGAGAAATTTAAGGGGAGAGACATACTAGATACTTACGTTTTATCGTCTGATTAT
-----+-----+-----+-----+-----+-----+ 13560
TTGTTCTCTTTAAATTTCCCTCTCTGTATGATCTATGAATGCAAATAGCAGACTAATA
a N K E K F K G R D I L D T Y V L S S D Y -

ORF9

13561 CCAGGGTTTAAATGAAGTTGCTTTTCGCTCCGCTATCTTATCTTAAGGTTGTCAAAGTCGC
-----+-----+-----+-----+-----+-----+ 13620
GGTCCCAAATTTACTTCAACGAAAGCGAGGCGATAGAATAGAATTCCAACAGTTTCAGCG
a P G F K *
c M K L L S L R Y L I L R L S K S L -

13621 TTAGAACGAACGATCACTTGGTTTTAATACTTATAAAGGAGGCGCTTATAAACTATTACA
-----+-----+-----+-----+-----+-----+ 13680
AATCTTGCTTGCTAGTGAACCAAAATTATGAATATTTCTCCGGAATATTTGATAATGT
c R T N D H L V L I L I K E A L I N Y Y N -

13681 ACGCCTCTTTTACCGATGAGGGTGCCGTATTAAGAGACTCTCGCGAAAGTATAGAGAATT
-----+-----+-----+-----+-----+-----+ 13740
TGCGGAGAAAGTGGCTACTCCACGGCATAATTCTCTGAGAGCGCTTTCATATCTCTTAA
c A S F T D E G A V L R D S R E S I E N F -

13741 TTCTCGTAGCCAGGTGCGGTTTCGCAAATTCCTGCCGAGTCATGAAGGCTTTGATCACTA
-----+-----+-----+-----+-----+-----+ 13800
AAGAGCATCGGTCCACGCCAAGCGTTTTAAGGACGGCTCAGTACTTCCGAACTAGTGAT
c L V A R C G S Q N S C R V M K A L I T N -

13801 ACACAGTCTGTAAGATGTCGATAGAAACAGCCAGAAGTTTTATCGGAGACTTAATACTCG
-----+-----+-----+-----+-----+-----+ 13860
TGTGTGACAGATTCTACAGCTATCTTTGTGGTCTTCAAAATAGCCTCTGAATTATGAGC
c T V C K M S I E T A R S F I G D L I L V -

13861 TCGCCGACTCCTCTGTTTCAGCGTTGGAAGAAGCGAAATCAATTAAAGATAATTTCCGCT
-----+-----+-----+-----+-----+-----+ 13920
AGCGGCTGAGGAGACAAAGTCGCAACCTTCTTCGCTTTAGTTAATTTCTATTAAAGGCGA
c A D S S V S A L E E A K S I K D N F R L -

13921 TAAGAAAAAGGAGAGGCAAGTATTATTATAGTGGTGATTGTGGATCCGACGTTGCCGAAAG
-----+-----+-----+-----+-----+-----+ 13980
ATTCTTTTTCTCTCCGTTTATAATAATATCACCCTAACACCTAGGCTGCAACGCTTTC
c R K R R G K Y Y Y S G D C G S D V A K V -

13981 TTAAGTATATTTTGTCTGGGGAGAATCGAGGATTGGGGTGCGTAGATTTCCTTGAAGCTAG
-----+-----+-----+-----+-----+-----+ 14040
AATTCATATAAAACAGACCCCTCTTAGCTCCTAACCCACGCATCTAAGGAAGTTTCGATC
c K Y I L S G E N R G L G C V D S L K L V -

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FIG. 18V

14041 TTTGCGTAGGTAGACAAGGAGGTGGAACGTACTACAGCACCTACTAATCTCATCTCTGG
-----+-----+-----+-----+-----+-----+ 14100
AAACGCATCCATCTGTTCCCTCCACCTTTGCATGATGTCGTGGATGATTAGAGTAGAGACC
C V G R Q G G G N V L Q H L L I S S L G -

ORF10

14101 GTTAAAGCATCATGGACCTATCGTTTATTATTGTGCAGATCCTTTCCGCCTCGTACAATA
-----+-----+-----+-----+-----+-----+ 14160
CAATTTTCGTAGTACCTGGATAGCAAATAATAACACGTCTAGGAAAGGCGGAGCATGTTAT
* M D L S F I I V Q I L S A S Y N N -

14161 ATGACGTGACAGCACTTTACACTTTGATTAACGCGTATAATAGCGTTGATGATACGACGC
-----+-----+-----+-----+-----+-----+ 14220
TACTGCACTGTCGTGAAATGTGAACTAATTGCGCATATTATCGCAACTACTATGCTGCG
D V T A L Y T L I N A Y N S V D D T T R -

14221 GCTGGGCAGCGATAAACGATCCGCAAGCTGAGGTTAACGTCGTGAAGGCTTACGTAGCTA
-----+-----+-----+-----+-----+-----+ 14280
CGACCCGTCGCTATTTGCTAGGCGTTGCACTCCAATTGCAGCACTTCCGAATGCATCGAT
W A A I N D P Q A E V N V V K A Y V A T -

14281 CTACAGCGACGACTGAGCTGCATAGAACAATTCTCATTGACAGTATAGACTCCGCCTTCG
-----+-----+-----+-----+-----+-----+ 14340
GATGTCGTGCTGACTCGACGTATCTTGTTAAGAGTAAGTGTATATCTGAGGCGGAAGC
T A T T E L H R T I L I D S I D S A F A -

14341 CTTATGACCAAGTGGGGTGTGTTGGTGGGCATAGCTAGAGGTTTGCTTAGACATTCCGAAG
-----+-----+-----+-----+-----+-----+ 14400
GAATACTGGTTCACCCACAAACCACCCGTATCGATCTCCAAACGAATCTGTAAGCCTTC
Y D Q V G C L V G I A R G L L R H S E D -

14401 ATGTTCTGGAGGTCATCAAGTCGATGGAGTTATTTCGAAGTGTGTCGTGGAAAGAGGGGAA
-----+-----+-----+-----+-----+-----+ 14460
TACAAGACCTCCAGTAGTTCAGCTACCTCAATAAGCTTCACACAGCACCTTTCTCCCCTT
V L E V I K S M E L F E V C R G K R G S -

14461 GCAAAAGATATCTTGGATACTTAAGTGATCAATGCACCTAACAAATACATGATGCTAACTC
-----+-----+-----+-----+-----+-----+ 14520
CGTTTTCTATAGAACCTATGAATTCAGTACGTGATTGTTTATGTACTACGATTGAG
K R Y L G Y L S D Q C T N K Y M M L T Q -

14521 AGGCCGGACTGGCCGAGTTGAAGGAGCAGACATACTACGAACGAATCATCTAGTCAGTG
-----+-----+-----+-----+-----+-----+ 14580
TCCGGCCTGACCGGCGTCAACTTCCTCGTCTGTATGATGCTTGCTTAGTAGATCAGTCAC
A G L A A V E G A D I L R T N H L V S G -

14581 GTAATAAGTTCTCTCCAAATTTCCGGATCGCTAGGATGTTGCTCTTGACGCTTTGTTGCG
-----+-----+-----+-----+-----+-----+ 14640
CATTATTCAAGAGAGGTTTAAAGCCCTAGCGATCCTACAACGAGAACTGCGAAACAACGC
N K F S P N F G I A R M L L L T L C C G -

14641 GAGCACTATAAAAAATGTTATGTTGTTTCAGCCAGTGTCAAATTTTCAAACGGGTTACAATT
-----+-----+-----+-----+-----+-----+ 14700
CTCGTGATATTTTACAATACAACAAGTCGGTCACAGTTTAAAAGTTTGCCCAATGTTAA
A L *

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FIG. 18W

14701 ATCGCTACTTATTTGCGCATGTTTGTAGCGGTGCTAATTGTTAGCTTTTGTAGAAGGCG
-----+-----+-----+-----+-----+-----+ 14760
TAGCGATGAATAAACGCGTACAAACAATCGCCACGATTAACAATCGAAAACATCTTCCGC

ORF11

14761 ATGAGGCACTTAGAAAAACCCATCAGAGTAGCGGTACACTATTGCGTCGTGCGAAGTGAC
-----+-----+-----+-----+-----+-----+ 14820
TACTCCGTGAATCTTTTTGGGTAGTCTCATCGCCATGTGATAACGCAGCACGCTTCACTG
a M R H L E K P I R V A V H Y C V V R S D -

14821 GTTTGTGACGGGTGGGATGTATTTATAGGCGTAACGTTAATCGGTATGTTTATTAGTTAC
-----+-----+-----+-----+-----+-----+ 14880
CAAACACTGCCCACCCTACATAAATATCCGCATTGCAATTAGCCATACAAATAATCAATG
a V C D G W D V F I G V T L I G M F I S Y -

14881 TATTTATATGCTCTAATTAGCATATGTAGAAAAGGAGAAGGTTTAACAACCAGTAATGGG
-----+-----+-----+-----+-----+-----+ 14940
ATAAATATACGAGATTAATCGTATACATCTTTTCCTCTTCCAAATTGTTGGTCATTACCC
a Y L Y A L I S I C R K G E G L T T S N G -

14941 TAAAAATCCTTCAATAAATTTGAAATAAACAAAAGTAAGAAAAATGAAATAATTAGGCTA
-----+-----+-----+-----+-----+-----+ 15000
ATTTTGTAGGAAGTTATTTAACTTTATTTGTTTTCATTCTTTTACTTTATTAATCCGAT
a * -

15001 GTCTTTTTGTTTCGTCTTTTCGCTTTTGTAGAATAGGTTTATTTTCGAGGTAAGATGACTAA
-----+-----+-----+-----+-----+-----+ 15060
CAGAAAAACAAGCAGAAAGCGAAAACATCTTATCCAAAATAAAGCTCCATTCTACTGATT

15061 ACTCTACCTCACGGTTTAATACTCTGATATTTGTAAAAATTAGTCCGTAAAGTCAGATAGT
-----+-----+-----+-----+-----+-----+ 15120
TGAGATGGAGTGCCAAATTATGAGACTATAAACATTTTAATCAGGCATTTCACTCTATCA

15121 GATATTATATTAGTATAGTATAATAAACGCCAAAATCCAATCAAAGTTTGGGACCTAGGC
-----+-----+-----+-----+-----+-----+ 15180
CTATAATATAATCATATCATATTATTTGCGGTTTATAGGTTAGTTTCAAACCCTGGATCCG

15181 GGGCCTCTTATGAGGCTAACTTATCGACAATAAGTTAGGTCCGCCAC
-----+-----+-----+-----+-----+-----+ 15227
CCCGGAGAATACTCCGATTGAATAGCTGTTATTCATCCAGGCGGTG

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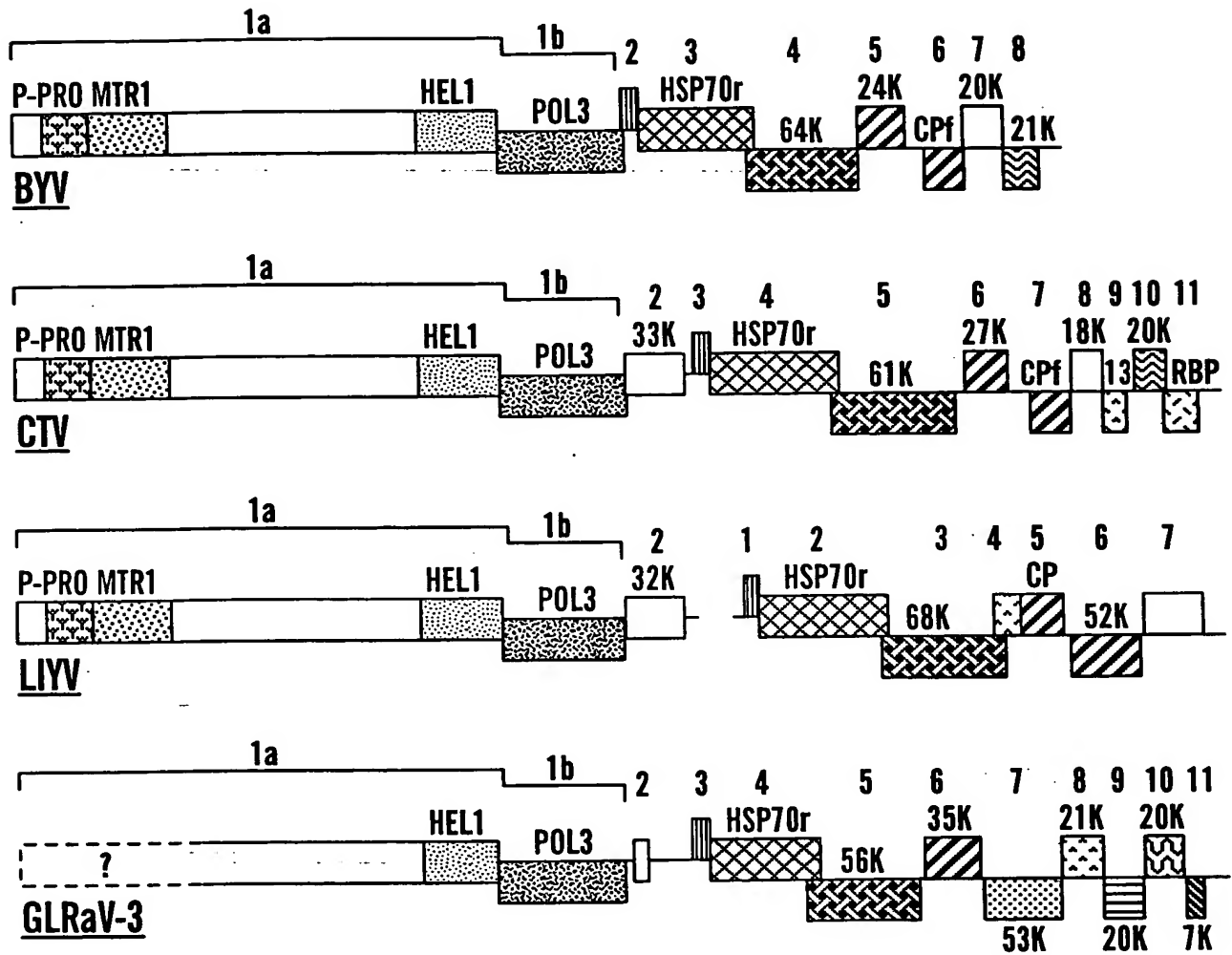


FIG. 19

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FIG. 20

I (A) Ia

BYV_HEL	FTFTNLSANV	LLYEAPPGGG	KTTTLIKVFC	ETFSK.VNSL	ILTANKSSRE
CTV_HEL	LTFTNEEHS	IVYEAPPGGG	KTHSLVNSYA	DYCVK.VSCL	VVTANKNSQT
GLRaV3_HEL	VGESFKSFEY	KCYNAPPGGG	KTT...MLV	DEFVKSPNST	ATITANVGSS
LIYV_HEL	MVRRPDVNG	KFYNKPPGAG	KTTTIAKLMS	KDLKNKVKCL	ALSYTKVGRL
CONSENSUS	----- --Y-aPPGaG KtT----- d-f-k-v--l -----k----				

II

BYV_HEL	EILAKVNRIV	LD...EGDTP	LQTRDRILTI	DSYLMNNG	LTCKVLYLDE
CTV_HEL	EISQRISNEL	MGRKLAAYV	TDAASRVFTV	DSYLMNHL.R	LTQQLLFIDE
GLRaV3_HEL	EDINM....A	VKKR...DPN	LEGLNSATTV	NSRVVNFIVR	GMKRVLVDE
LIYV_HEL	ELIDKLKKG	IEKP...EKY	VKTYDSFLMN	NDNILEIV..NLYCDE
CONSENSUS	E----- -d-- -----ltv -s--mn---- -----ly-DE				

III

BYV_HEL	CFMVHAGAAV	ACIEFTKCD	AILFGDSRQI	RYGRCSLDT	AVLSDLNRFV
CTV_HEL	CFMVHAGAIG	AVVEFTSCKA	VVFFGDSKQI	HYIHRNDLGV	SFVADIDAFI
GLRaV3_HEL	VYMMHQG.LL	QLGVFQPA	GLFFGDINQI	PFINREKVFR	MDCA..VXLP
LIYV_HEL	VFMMHAGHFL	TLLTKIAYQN	GYCYGDVNQI	PFINRDPYTP	AYLS..REFF
CONSENSUS	-fM-HaG--- ----f--c-- --ffGD--QI --i-r----- ----f-				

IV

BYV_HEL	DDESRVYGEV	SYRCPWDVCA	WLSTF.....	...YPKTVAT	TNLVSAGQSS
CTV_HEL	QPEHRIYGEV	SYRCPWDICE	WLSEF.....	...YPRH VAT	ANVGSIGKSS
GLRaV3_HEL	KKESVVYTSK	SYRCPDVCY	LLSSMTVRGT	EKCYPEKVVS	GKDK.PVVR
LIYV_HEL	RKQDLNYDTY	TYRCPDTCY	LLSNLKDEMG	NIIYAGGVKN	VNEVYPTIRS
CONSENSUS	--e--vY--- SYRCP-DvC- -LS-f----- ---Yp--V-- -n-----S				

V

BYV_HEL	MQVREIESVD	DVEYSSEFVY	LTMLQSEKGD	LLKSFGK..R	SRSSVEKPTV
CTV_HEL	VSIEEINGCD	DVPYDKAAKY	IVYTQAEKND	LQKHLGRITV	GRNKV.VPIV
GLRaV3_HEL	LSKRPIGTTD	DVAEINADV	LCMTQLEKSD	MKRSKLGKGG	.ETP.....V
LIYV_HEL	LNLFGINVVG	EVPVEYNAKY	LTFTQDEKLN	LQRHIDSQGG	CRNA.....V
CONSENSUS	l----I---d dV-----Y l--tQ-EK-d l---l----- -r-----V				

VI

BYV_HEL	LTVHEAQGET	YRKVNLRVTK	FQEDDPFRSE	NHITVALSRH	VESLTYSVLS
CTV_HEL	NTVHEVQGET	YKRVLRVRFK	YQEDTPFSSK	NHIVVALTRH	VDSLVSIVLT
GLRaV3_HEL	MTVHEAQGKT	FSDVVLFR TK	KADDSLFTKQ	PHILVGLSRH	TRSLVYAALS
LIYV_HEL	STVNEAQGCT	FSEVNLVRLV	QFDNPVMSDI	NQFVVAISRH	TTTFKYFTPH
CONSENSUS	-TVhEaQG-T ---V-LvR-k ---d--f--- nhi-ValsRH --sl-Y--l-				

VII

BYV_HEL	SKRDDAIAQA	I
CTV_HEL	SRRYDDTATN	I
GLRaV3_HEL	SELDDKVGTY	I
LIYV_HEL	SRLNDRVSNA	I
CONSENSUS	S---D-v--- I	

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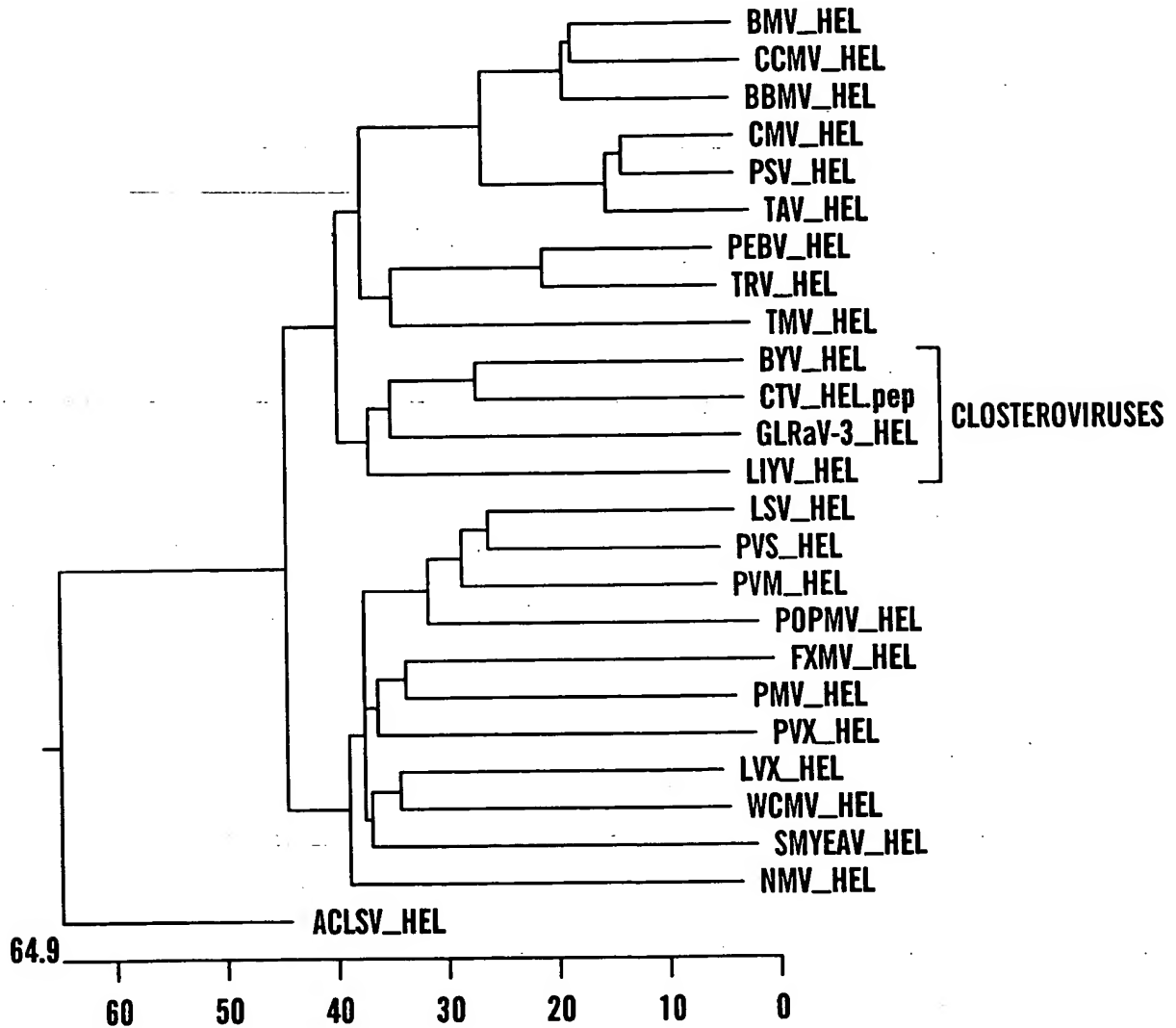


FIG. 21

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FIG. 22

	I		II	
BYV_RdRp	ITTFKLMVKR	DAKVKLDSSC	LVKHPPAQNI	MFHRKAVNAI
CTV_RdRp	ISNFKLMVKR	DAKVKLDDSS	LSKHPPAQNI	MFHKKFINAI
GLRaV3_RdRp	LTSYTLMVKA	DVKPKLDNTP	LSKYVTGQNI	VYHRCVTAL
LIYV_RdRp	FKTLNLMVKG	ETKPKMDLST	YDSYNAPANI	VYYQQIVNLY
CONSENSUS	---f-LMVK-	d-K-KlD-s-	l-k----qNI	--h---vna- FSp-F-e---
	III		IV	
BYV_RdRp	RVITCTNSNI	VFFTEMTNST	LASIAKEMLG	.SEHVYNVGE
CTV_RdRp	RVLSSLNDNI	VFFTEMTNAG	LAEIIRRIIG	.DDDNLFVGE
GLRaV3_RdRp	RLKYVVDERW	LFYHGMDTAE	LAXALRNNLG	.DIRQYYTYE
LIYV_RdRp	RLTYCLSDKI	VLYSGMNTDV	LAELIESKLP	LGLNAYHTLE
CONSENSUS	R-----d-i	vf---M----	LA-----lg	-----y---E idfSKfDKSQ
BYV_RdRp	DAFIKSFERT	LYSAFGFDED	LLD.VWMOGE	YTSNATTLDG
CTV_RdRp	DLFIKEYERT	LYSEFGFDTE	LLD.VWMEGE	YRARATTLDG
GLRaV3_RdRp	SALMKQVEEL	ILLTLGVDRE	VLS.TFFCGE	YDSVVRTMTK
LIYV_RdRp	GTCFKLYEEM	MYKMFGFSPE	LYDRDFKYTE	YFCRAKA.TC
CONSENSUS	--f-K-yE--	ly--fGfd-e	lld-----gE	Y---a-tl-- -l--sv--QR
	V		VI	
BYV_RdRp	KSGASNTWIG	NSIETLGILS	MFYYTNRFKA	LFVSGDDSLI
CTV_RdRp	RSGGSNTWIG	NSLVTLGILS	LYYDVSKFDL	LLVSGDDSLI
GLRaV3_RdRp	RSGGANTWLG	NSLVLCTLLS	VVLRGLDYSY	IVVSGDDSLI
LIYV_RdRp	RTGSPNTWLS	NTLVTLGMLL	SSYDIDDIDL	LLVSGDDSLI
CONSENSUS	rsG--NTW-G	Nslvtlg-ls	--y----f--	llVSGDDSLI fS-----n--
	VII		VIII	
BYV_RdRp	DAMCTELGFE	TKFLTSPVPY	FCSKFFVMTG	HDVFFVPDPY
CTV_RdRp	SEICLETGFE	TKFMSPSPY	FCSKFVVQTG	NKTCFVPDPY
GLRaV3_RdRp	SVLSDNFGFD	VKIFNQAAPY	FCSKFLVQVE	DSLFFVPDPL
LIYV_RdRp	QEINKNFGME	AKYIEKSSPY	FCSKFIVELN	GKLKVIPDPI
CONSENSUS	-----fgfe	-Kf---s-PY	FCSKF-V---	----fvPDP- kl-vKlga--
BYV_RdRp	..KDEVDDDEF	LFEVFTSFRD	LTKDLVDERV	IELLTHLVHS
CTV_RdRp	..QNKLTDVE	LFELFTSFKD	MTQDFGDQVV	LEKLKLLVEA
GLRaV3_RdRp	..KTSIDID.L	LHEIFQSFDV	LSKGFNREDV	IQELAKLVTR
LIYV_RdRp	RQEDFVNGSV	VKERFISFKD	LMKEYDNDVA	VIRIDEAVCY
CONSENSUS	-----d--	l-E-F-SF-D	l-kdf--e-v	i--l--lv-- ky---sG-ty
BYV_RdRp	AALCAIH CIR	SNFSSFKKLY		
CTV_RdRp	PALCAIH CVR	SNFLSFERLF		
GLRaV3_RdRp	SALCVLHVLS	ANFSQFCRLY		
LIYV_RdRp	AALCYIHCCM	SNFVSFRRIY		
CONSENSUS	-ALC-iHc--	sNF-sF-rly		

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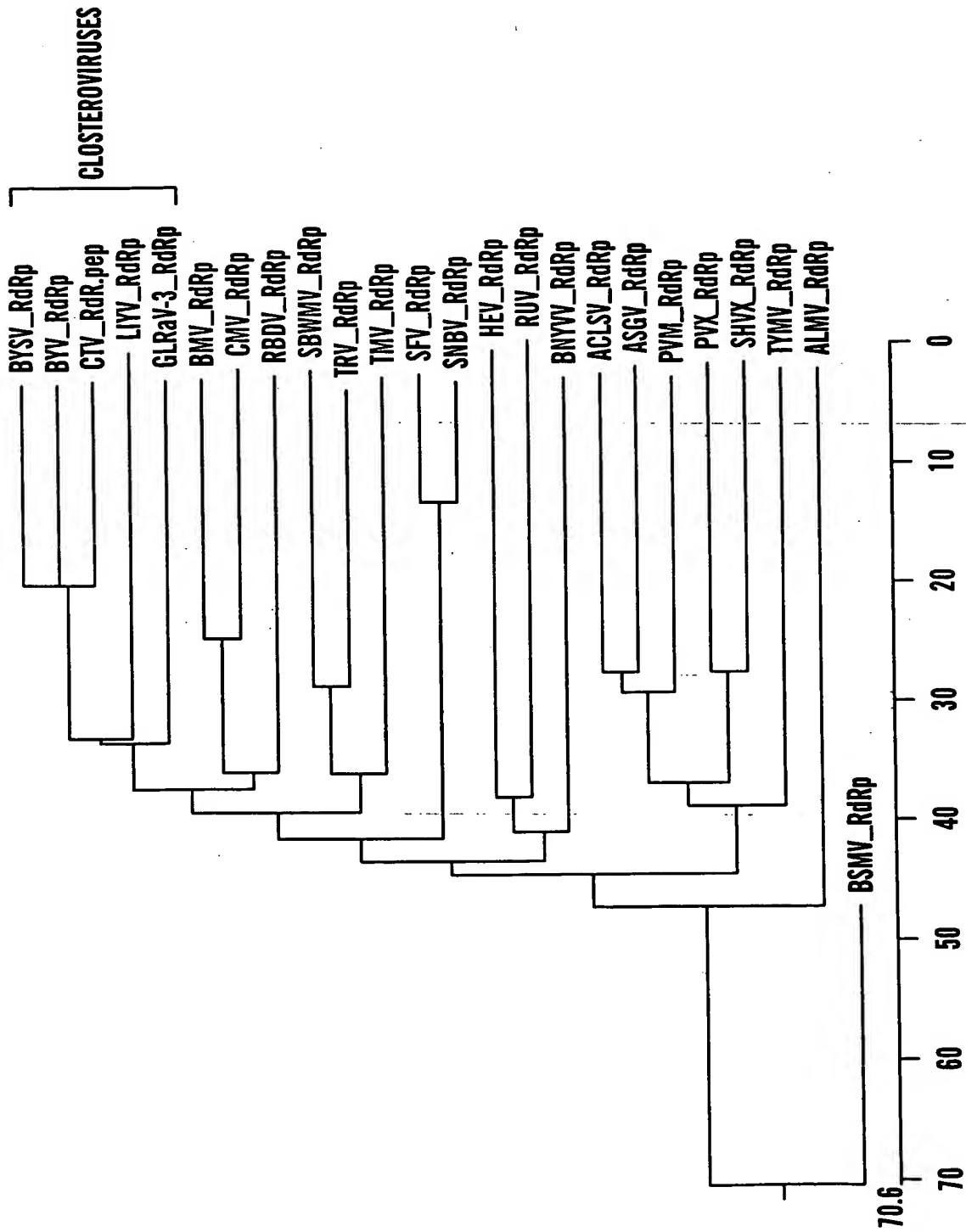


FIG. 23

FIG. 24

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transmembrane

1 54
BYV_p7K MDCVLRSYLL LAFGELICLF LFCLVFIFWF VYKQILFRTT AQSNEARHNH STTV*
LIV_p5K MSILLFFL MSILVWFIFT ILKLLFVNTD SEVNIPNKS R F* ...
GLRaV3_p5K MDD FKQAILLLV DFVFIILLL VLTFFVPRLQ QSSTINTGLR TV*..
CTV_p6K MDCVIQGLT FLVGIAVFCA FAGLIIVIT IYRCTIKPVR SASPYGTHAT V* ...
CONSENSUS ----- f---il-f-- ---lvi-i-- -----s-----

FIG. 25

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FIG. 26A

A					
BYV_p65	..MVVFGLDF	GTTFSSVCAY	VGEELYLFKQ	RDSAYIPTV	FLHSDTQEVA
CTV_p65	..MVLLGLDF	GTTFSTVAMA	TPSELVILKQ	SNSSYIPTCL	LLHAEPNSVS
GLRaV3_p59	...MEVGIDF	GTTFSTICFS	PSGVSGCTPV	AGSVYVETQI	FIPEGSSSTYL
LIYV_p62	MRDCKVGLDF	GTTFSTVSTL	VNNSMYVLRL	GDSAYIPTCI	AITPGGEAI.
CONSENSUS	-----GIDF	GTTFStv---	----l--l--	--S-YipTci	f-----v-
BYV_p65	FGYDAEVLNS	DLSVRGGFYR	DLKRWIGCDE	ENYRDYLEKL	KPHYKTELLK
CTV_p65	YGYDAEYLAA	S.GESGSFYK	DLKRWVGCTA	KNYQTYLHKL	SPSYKVIVKE
GLRaV3_p59	IG.KAAGKAY	RDGVEGRLYV	NPKRWVGVTR	DNVERYVEKL	KPTYTVKM..
LIYV_p62	IGGAAEVLSG	DDTPHCFYF.	DLKRWVGVD	NTFKFAMNKI	RPKYVAELVE
CONSENSUS	-G--Ae-l--	-----g-fY-	dlKRWvG---	-ny--yl-Kl	-P-Y---l--
BYV_p65	VAQSSKSTVK	LDCYSGTVPQ	NATLPGLIAT	FVKALISTAS	EAFKCQCTGV
CTV_p65	FGTKSVFPVY	LSPLNNDLGL	SVALPSLIAS	YAKSILSDAE	RVFNVSCTGV
GLRaV3_p59	...DSGGALL	IGGLSGSPDT	LLRVVDVICL	FLRALILECE	RYTSTTVTAA
LIYV_p62GEVY	LTGINKGFSI	KLSVKQLIKA	YIETIVRLLA	SSYSLRVIDL
CONSENSUS	----s-----	l-----	-----lI--	-----i----	--f----T--
B			D		
BYV_p65	ICSVPANYN	LQRSFTESC	NLSGYPCVYM	VNEPSAAALS	ACSRIKGATS
CTV_p65	ICSVPAGYNT	LQRAFTQQSI	MSGYSCVYI	INEPSAAAYS	TLPKLNSADK
GLRaV3_p59	VVTVPADYNS	FKRSFVVEAL	KGLGIPVRGV	VNEPTAAALY	SLAKSRVEDL
LIYV_p62	NQSVPADYKN	AQRLAARSVL	KALSFPCRR	INEPSAAAVY	CVSRYPNYNY
CONSENSUS	i-sVPA-Yn-	lqR-f-----	---gypc--i	-NEPsAAA--	-----
C			D		
BYV_p65	PVLVYDFGGG	TFDVSVISAL	NNTFVVRASG	GDMNLGGRDI	DKAFVEHLYN
CTV_p65	YLAVYDFGGG	TFDVSIVSVR	LPTFAVRSSS	GDMNLGGRDI	DKKLSDKIYE
GLRaV3_p59	LLAVFDFGGG	TFDVSFVKKK	GNILCVIFSV	GDNFLGGRDI	DRAIVEVIKQ
LIYV_p62	FL.VYDFGGG	TFDVSLIGKY	KSYVTVIDTE	GDSFLGGRDI	DKSIEDYLVG
CONSENSUS	-l-VyDFGGG	TFDVS-----	---f-V--s-	GD--LGGRDI	Dk-----
BYV_p65	KAQ...LPVN	YKIDISFLKE	SLSKKVSFLN	FPVSEQGVR	VDVLNVNSEL
CTV_p65	MAD...FVPQ	KELNVSSLKE	ALSLQTDPAK	YT.VNHYGMS	ETVSIQDTVL
GLRaV3_p59	KIKGASDAK	LGIFVSSMKE	DLSNNNAITQ	HLIPVEGGVE	V.VDLTSDLE
LIYV_p62	KYNIKKVIP.	.ATYLALIKE	E.CNNTNKS	FTILFDDGSV	QVVEFSKSEL
CONSENSUS	k-----	----vs-lKE	-ls-----	f-i--e-G--	--V-----eL
E					
BYV_p65	AEVAAPFVER	TIKIVKEVY.	.EKYCSSLRL	EPNVKAKLLM	VGGSSYLPGL
CTV_p65	REIASVFINR	TIDILTQV..	..KVKSSMPE	SQSL..KLVV	VGGSSYLPGL
GLRaV3_p59	DAIVAPFSAR	AVEVFKTGP.	.DNFYPPDVI	A.....VM	TGGSSALVKV
LIYV_p62	EKCVRPFVER	SIKLINDVVV	RNKLTSGV..IYM	VGGSSLLQPV
CONSENSUS	--i--pFv-R	-i-i---v--	--k--s----	-----m	vGGSS-L---

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FIG. 26B

F

BYV_p65	LSRLSSIPFV	DEC.L.VLPD	ARAAVAGGCA	LYSACLRNDS	PMLLVDCAAH
CTV_p65	LDALATVPFV	SGI.V.PVED	ARTAVARGCA	LYSECLDGRS	KALLIDCITH
GLRaV3_p59	RSDVANLPQI	SKV.VFDSTD	FRCSVACGAK	VYCDTLAGNS	GLRLVDTLTN
LIYV_p62	QDMVRSYAST	KGLTLVADQD	MRSVAVSYGCS	VLHK.LEDNK	EIVYIDCNSH
CONSENSUS	-----p-v	-----D	-R-aVa-Gc-	-y---L---s	---l-Dc--h

G

BYV_p65	NLSISSKYCE	SIVCVPAAGSP	IPFTGVRTVN	MTGSNASAVY	SAALFEGDFV
CTV_p65	HLSVTTF SAD	SVVVAAAGSP	IPFEGERKLT	LRKCVSTSNY	QARMFEGDYE
GLRaV3_p59	TLTDEVVGLQ	PVVIFPKGSP	IPCSYTHRYT	V....GGGDV	VYGIFEGE..
LIYV_p62	PLSDISFNCD	PEPIIRKPMS	IPYHTTVKMR	HDRPLKT...	IVNIYEGSNL
CONSENSUS	-Ls-----d	-vvi---gsp	IPf-----	-----	----fEGd--

H

BYV_p65	KCRLNKRIFF	GDVVLGNVGV	TGSATRTVPL	TLEINVSSVG	TISFSLVGPT
CTV_p65	KVFRNERIYA	ASVSLFTLG	NWSVPNDVEM	TLVTKVDSMG	KVEFYLGKPS
GLRaV3_p59NNRAFL	NEPTFRGVSK	RRGDPVETDV	A.QFNLSTDG	TVSVIVNGEE
LIYV_p62	FMPENDWLIS	SNINTTDFAKVGEEY	SKVYEYDIDG	IITLKIRNEV
CONSENSUS	---N-r-f-	--v-l-----	-----e-	-----G	---f---g--

BYV_p65	GVKKLIGGNA	AYDFSSYQLG	ERVVADLHKH	NSDKVKLIHA	LTYQPFQRKK
CTV_p65	GELVNVQGTS	HYDYAGMPHP	TRKLVRLSDY	NVNSAALVLA	LTLTREKREK
GLRaV3_p59	VKNEYLVPGT	TNVLDSL...	...VYKSGRE	DLEAKAIPY	LTTLNILHDK
LIYV_p62	TGKMFTLPNS	FTKSDNIKPI	TFKLTQLSNT	D.DLATLTSL	LGYHDKNFER
CONSENSUS	-----	-----	-----l---	--d---l---	Lt-----ek

BYV_p65	LTDGDKALFL	KRLTADYRRE	ARKFSSY...DDAV	LNSSELLLGR
CTV_p65	FLLRT...LF	DTLLADLRKT	A.SLSEYSKK	YPITRNDIDV	VSSR...MGI
GLRaV3_p59	AFTRNLGNK	DKGFSDLRIE	ENFLKS....	...AVDTDTI	LNG*.....
LIYV_p62	FYG.....L	FNVPTILIKE	IDKLGGFKTL	YRRLKSMNAN	F.....
CONSENSUS	f-----l	-----dlr-e	---l--y---	-----v	l-----

BYV_p65	IIPKILRGSR	VEKLDV*
CTV_p65	VVSKVLRGSD	LERIPL.
GLRaV3_p59
LIYV_p62
CONSENSUS	-----	-----

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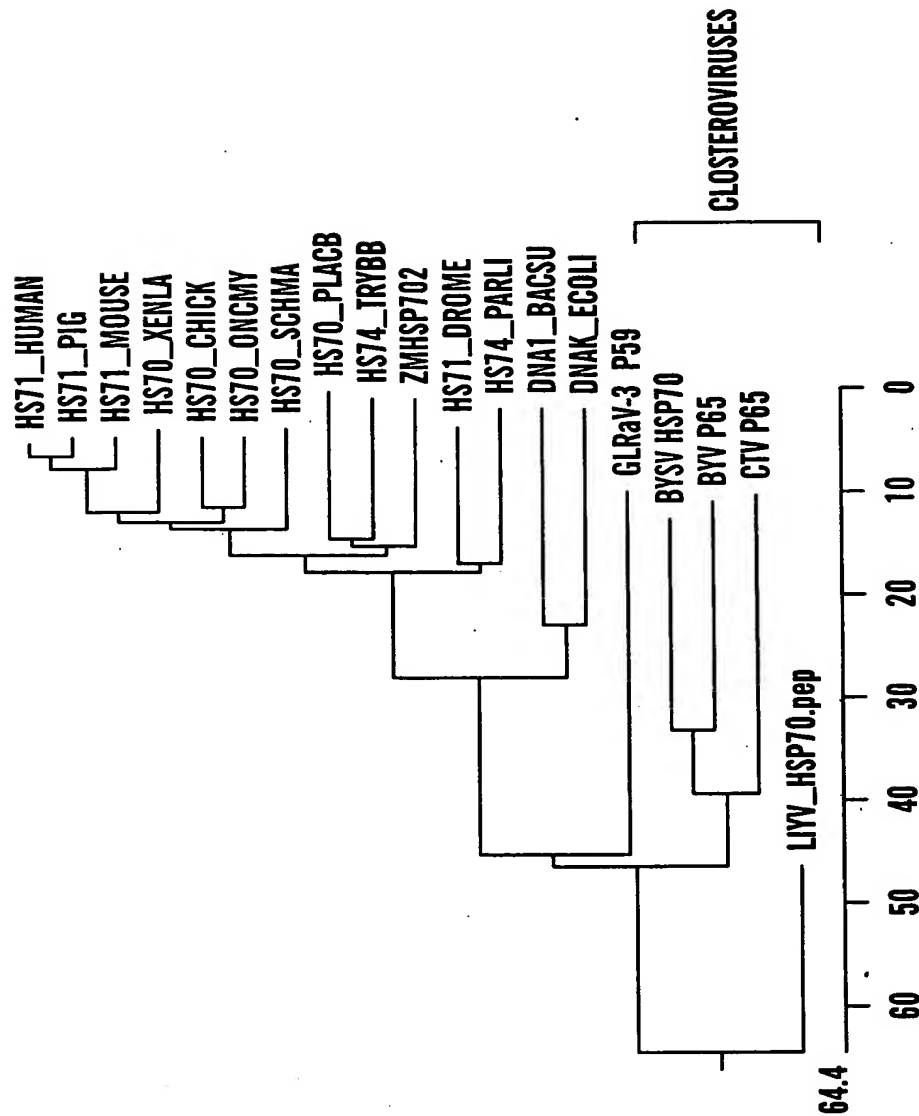


FIG. 27

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FIG. 28A

```

BYV_p61  MTTRFSTPAN YYWGELFRRF FGGQEW.... .KNLMSE AASVSRPRYS
CTV_p61  .....MSSH HVWGSFLRFK YGEAIW.... .KEYLSE STRNFDERNV
LIYV_P59  ..MLNDRIAV TCFQTLLKKS NVKHEMEQTN NYIVNNLADI NRNTFPALAG
GLRaV3_p55 .....MDK YIYVTGI..L NPNEARDEVF SVVNKGYIGP GGRSFSNRGS

```

CONSENSUS ----- --w--lf--f -----w---- ----k----- ----f--r--

```

BYV_p61  S.DFRFSDGV ILSRKTFGES TGES..FVRE FSLLLTFPKT YEVCKLCGVA
CTV_p61  SLDHTLSSGV VVRQSLNNA PQGT..FENE LALLYNSVVI NDFVELTGMP
LIYV_P59  SVRIDFNSDY YISGGQIVVS PKDSNAYVKL LIVYLKYCYI N.YSAKTKYP
GLRaV3_p55 KYTVVWEN.. ..SAARISGL TSTSQSTIDA FAYFL..... ..LKGGLTTT

```

CONSENSUS s----f---- --s----- ---s--fv-- ---ll-----

```

BYV_p61  MELALNGMN. .RLSDYNVSE FN.....IV DVKTVGCKFN IQSVTEFVKK
CTV_p61  LKSLMTGIED RKVPD....E LI.....SV DPHEVGCRFT LNDVESYLSM
LIYV_P59  PQSLLAFLDY DSFKAKWKY LDKSLTDYLD DNKTEGCSFT EQQVVEKYPQ
GLRaV3_p55 LSNPINCENW VRSSKDLSAF FRTLIKGIY ASRSVDSNLP KKDRDDIME.

```

CONSENSUS 1---l----- ----- d---vgc-f- ---v-e----

```

BYV_p61  INGVAEPSL VEHCWSLSNS CGELINPKDT KRFVSLIFKG KDLAESTDEA
CTV_p61  RGEDFADLAA VEHSWCLSNS CSRLLSSTEI DANKTLVF.T KNFDSNISG.
LIYV_P59  VDLSLVAKIL. ....YRVCNS LGKLLDLKDF ENKNISGFEI NTAQDSPTVA
GLRaV3_p55 .ASRRLSPSD AAFCAVSVQ VGKYVDVTQN LESTIVPLRV MEIKKRRGSA

```

CONSENSUS -----a---- ----w--sns -g-l----d- -----f-- -----a

```

BYV_p61  IVS..SSYLD YLSHCLNLYE TCNLSSNSGK KSLYDEFLKH VIDYL...EN
CTV_p61  .VT..TKLET YLSYCISLYK KHCM.KDDDY FNLILPMFNC LMKVL...AS
LIYV_P59  DDN..ES.ND FFRECVDNR YYSSLGSKL GKAKLEANAY IFKILLKSAS
GLRaV3_p55 HVSLPKVSA YVDFYTNLQE LLSDEVTRAR TDTVSAYATD SMAFLVKMLP

```

CONSENSUS -v----- yl--c-nl-- ----- ----L-----

```

BYV_p61  SDLEYRSPSD NPLVAGILYD MCFEYNTLKS TYLKNIESFD CFLSLYLPLL
CTV_p61  LGLFYEKHAD NPLLTGMLIE FCLENKVYYS TFKVNLNVR LFKSKVLPV
LIYV_P59  GEFDIDRLSR NPLAISKFMN LYTNHVTDS TFKSKFEALK SIKTPFASFI
GLRaV3_p55 LT.....AR EQWLKDVLYG LLVRRRPANF SYDVRVAWVY DVIATLKLVI

```

CONSENSUS --l----- npl----l-- lc----- t-----e--- -----i

```

BYV_p61  SEVFSMNWER PAPDVRLLE LDAAELLLKV PTINMHDST. ..FLYKNKLR
CTV_p61  LTVWDISEPD DPVDERVLIP FDPTDFVLDL PKLNIHDTM. ..VVVGNQIR
LIYV_P59  KKAFGIR... ..LN FEDSKIFYAL PKERQSDVLS DDMVESIVR
GLRaV3_p55 RLFFNKDTPG GIKDLKPCVP IESFDPFHEL S.....SYFS

```

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FIG. 28B

BYV_p61	YLESYFEDDS	NELIKVKVDS	LLTRDNPEL.	.KLAQRWV..	...GFHCYYG
CTV_p61	QLEYVVESDA	LDDLSQHVDL	RLAADNPDL.	.RVGLRWA..	...GMFVYYG
LIYV_P59	DAASFTVVSD	NNYLPERVDR	FVTQLLLELF	PKTKASFPNK	IMFGFLHYFA
GLRaV3_p55	RLSYEMTTGK	GGKICPEIAE	KLVRRLMEEN	YKLRLT.PVM	ALIIILVYYS
CONSENSUS	-l-----	-----vd-	-l-----el-	-k----w---	---g-l-Yy-

	II				
BYV_p61	VFRTAQTRKV	KRDAEYKLPP	AL.....GE	FVINMSGVEE	FF.EELQKKM
CTV_p61	VYRCVVDRAV	ERPTLFRLPQ	KLLSQDDGES	CSLHMGSVEA	LF.NLVQKVN
LIYV_P59	LSTTNSKR..FNDTQ	ESTIEIEGET	LKISLKFITS	YLRNAIQSQH
GLRaV3_p55	IYGTNATRIK	RRPDFLNTRI	KGRVE.....	.KVSLRGVED	..RAFRISEK
CONSENSUS	vy-t---R--	-r---f----	-----	--i----ve-	-f----q---

BYV_p61	PSI...SVRR	RFCGSLSHEA	FSVFKRFGVG	FPPITRLNVP	VKYSYLNVDY
CTV_p61	KDI...NVR	QFMGRHSEVA	LRLYRNLGLR	FPPISSVRLP	AHHGYLYVDF
LIYV_P59	PDYADSNIVR	LWCNKRSNLA	LGYFKSRNIQ	LYLYS..KYP	RLLNYMRFDY
GLRaV3_p56	RGINAQRVLC	RYYSDLTCLA	RRHYGIRRN	WKTLSYVD..	GTLAYDTADC
CONSENSUS	--i----v-r	-fc---s--A	l-----	f---s----p	----Yl--Dy

BYV_p61	YRHVKRVGLT	QDELTILSNI	EFDVAEMCCE	REVALQARRA	QR....GEKP
CTV_p61	YKRVPDGAVT	ADELESLRQL	RSSVDMCKD	R.VSITPPPF	NRLRRGSSRT
LIYV_P59	FKGLDMGKLT	DEERLSIQTL	RCITEDRS.E	GTLATHNDLN	SWILRP....
GLRaV3_p55	ITSKVRNTIN	TADHASIIHY	IKTNENQVTG	TTLPHQL*..
CONSENSUS	y-----t	-de--s----	----e----e	-----	-r-----

BYV_p61	FQGWKGTKNE	ISPCHARSSIR	VKKNNDSLNN	ILWKDVGARS	QRRNLNPLHRK
CTV_p61	FRGR.GARGA	SSRHMSRDVA	TSGFNLPYHG	RLYSTS*...
LIYV_P59
GLRaV3_p55
CONSENSUS	-----	-----	-----	-----	-----

BYV_p61	H*
CTV_p61	..
LIYV_P59	..
GLRaV3_p55	..
CONSENSUS	--

(5' primer, 93-224)

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FIG. 29A

NcoI

tacttatctagaacc

ATGGAAGCGAGTCGACGACTA
 ATGGAAGCGAGTCGACGACTATCGCCATCGGACGCCGCTTTTGCAGAGCAGTGTGGTT
 9404-----+-----+-----+-----+-----+-----+-----+-----
 M E A S R R L S P S D A A F C R A V S V -
 CAGGTAGGGAAGTATGTGGACGTAACGCAGAATTTAGAAAGTACGATCGTGCCGTTAAGA
 -----+-----+-----+-----+-----+-----+-----+-----
 Q V G K Y V D V T Q N L E S T I V P L R -
 GTTATGGAAATAAAGAAAAGACGAGGATCAGCACATGTTAGTTTACCGAAGGTGGTATCC
 -----+-----+-----+-----+-----+-----+-----+-----
 V M E I K K R R G S A H V S L P K V V S -
 GCTTACGTAGATTTTTTATACGAACTTGCAGGAATTGCTGTCTGGATGAAGTAACTAGGGCC
 -----+-----+-----+-----+-----+-----+-----+-----
 A Y V D F Y T N L Q E L L S D E V T R A -
 AGAACCGATACAGTTTCGGCATAACGCTACCGACTCTATGGCTTTCTTAGTTAAGATGTTA
 -----+-----+-----+-----+-----+-----+-----+-----
 R T D T V S A Y A T D S M A F L V K M L -
 CCCCTGACTGCTCGTGAGCAGTGGTTAAAAGACGTGCTAGGATATCTGCTGGTACGGAGA
 -----+-----+-----+-----+-----+-----+-----+-----
 P L T A R E Q W L K D V L G Y L L V R R -
 CGACCAGCAAATTTTTCCTACGACGTAAGAGTAGCTTGGGTATATGACGTGATCGCTACG
 -----+-----+-----+-----+-----+-----+-----+-----
 R P A N F S Y D V R V A W V Y D V I A T -
 CTCAAGCTGGTCATAAGATTGTTTTTCAACAAGGACACACCCGGGGGTATTAAAGACTTA
 -----+-----+-----+-----+-----+-----+-----+-----
 L K L V I R L F F N K D T P G G I K D L -
 AAACCGTGTGTGCCTATAGAGTCATTTCGACCCCTTTCACGAGCTTTCGTCCTATTTCTCT
 -----+-----+-----+-----+-----+-----+-----+-----
 K P C V P I E S F D P F H E L S S Y F S -
 AGGTAAAGTTACGAGATGACGACAGGTAAAGGGGAAAGATATGCCCCGAGATCGCCGAG
 -----+-----+-----+-----+-----+-----+-----+-----
 R L S Y E M T T G K G G K I C P E I A E -
 AAGTTGGTGCGCCGTCTAATGGAGGAAAACCTATAAGTTAAGATTGACCCCAGTGATGGCC
 -----+-----+-----+-----+-----+-----+-----+-----
 K L V R R L M E E N Y K L R L T P V M A -

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FIG. 29B

TTAATAATTATACTGGTATACTACTCCATTTACGGCACAAACGCTACCAGGATTAAAAGA

-----+-----+-----+-----+-----+-----+-----+-----+-----
L I I I L V Y Y S I Y G T N A T R I K R -

CGCCCCGATTTCCTCAATGTGAGGATAAAGGGAAGAGTCGAGAAGGTTTCGTTACGGGGG

-----+-----+-----+-----+-----+-----+-----+-----+-----
R P D F L N V R I K G R V E K V S L R G -

GTAGAAGATCGTGCCTTTAGAATATCAGAAAAGCGCGGGATAAACGCTCAACGTGTATTA

-----+-----+-----+-----+-----+-----+-----+-----+-----
V E D R A F R I S E K R G I N A Q R V L -

TGTAGGTACTATAGCGATCTCACATGTCTGGCTAGGCGACATTACGGCATTCGCAGGAAC

-----+-----+-----+-----+-----+-----+-----+-----+-----
C R Y Y S D L T C L A R R H Y G I R R N -

AATTGGAAGACGCTGAGTTATGTAGACGGGACGTTAGCGTATGACACGGCTGATTGTATA

-----+-----+-----+-----+-----+-----+-----+-----+-----
N W K T L S Y V D G T L A Y D T A D C I -

ACTTCTAAGGTGAGAAATACGATCAACACCGCAGATCACGCTAGCATTATACACTATATC

-----+-----+-----+-----+-----+-----+-----+-----+-----
T S K V R N T I N T A D H A S I I H Y I -

AAGACGAACGAAAACCAGGTTACCGGAACTACTCTACCACACCAGCTTTAAAGCTGCGTG

-----+-----+-----+-----+-----+-----+-----+-----+-----
K T N E N Q V T G T T L P H Q L *

TAGTATGCGACGATGTTTCT

-----+-----+-----+-----+-----+-----+-----+-----+-----
10503

ATCATACGCTGCTACAAAGA

ggtacctaggagttct

NcoI

(3' primer, 93-225)

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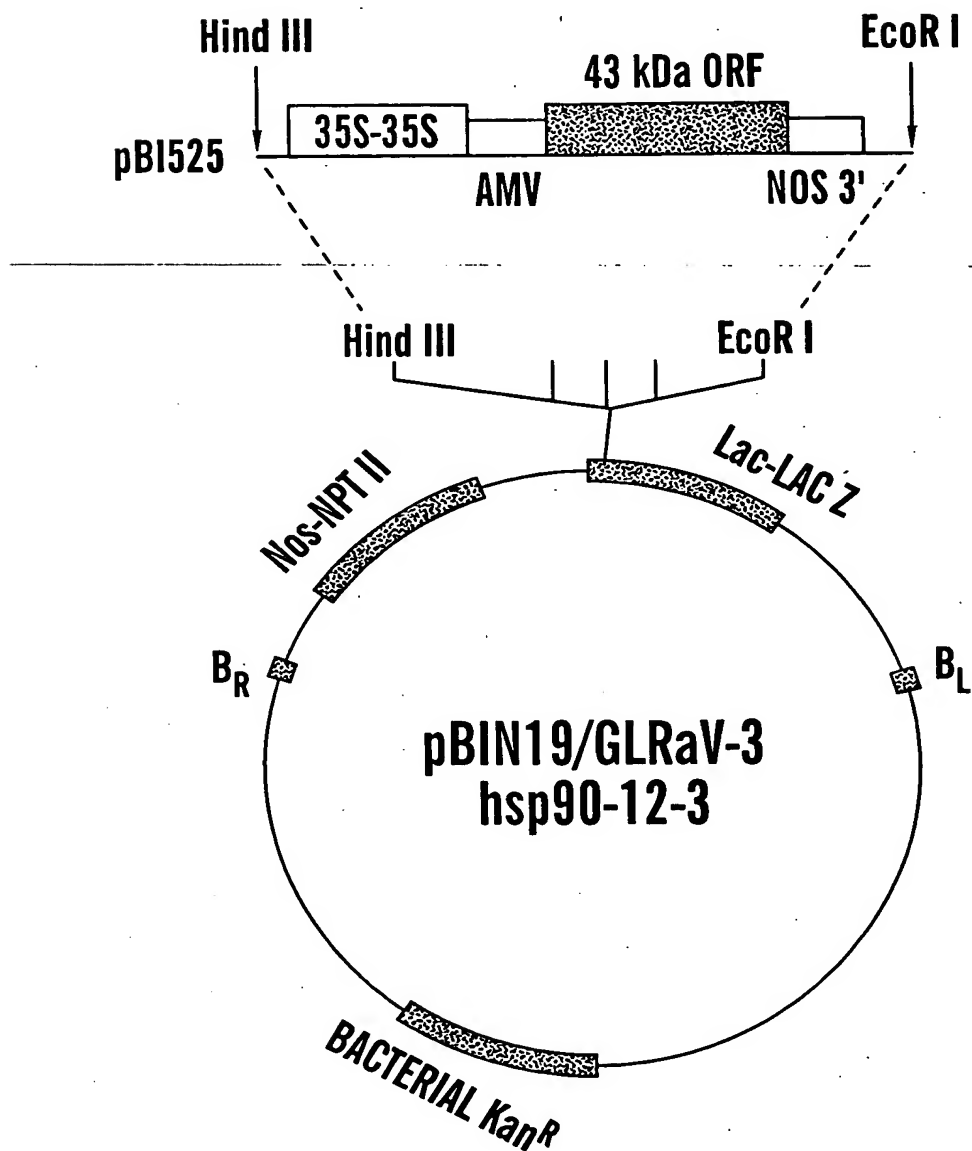


FIG. 30

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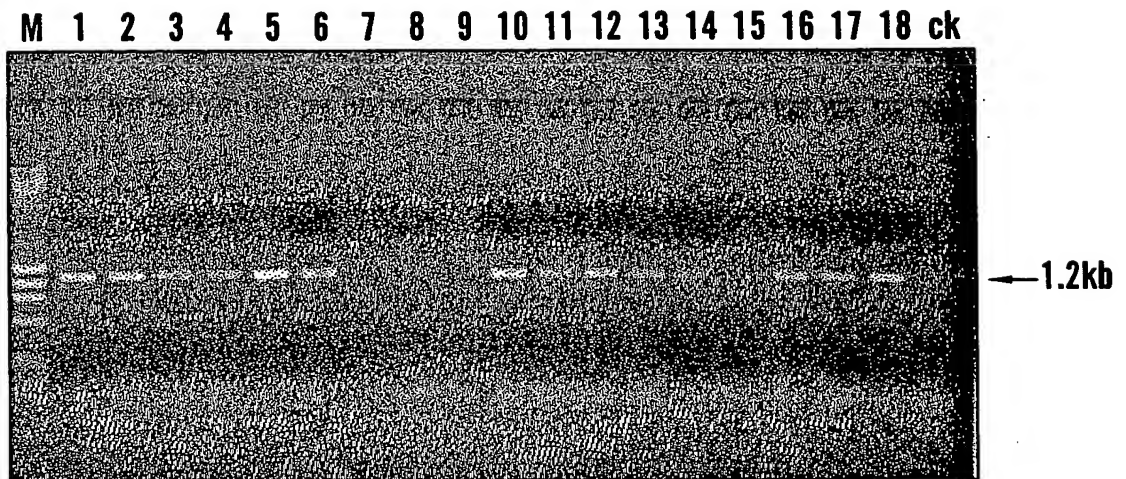


FIG. 31

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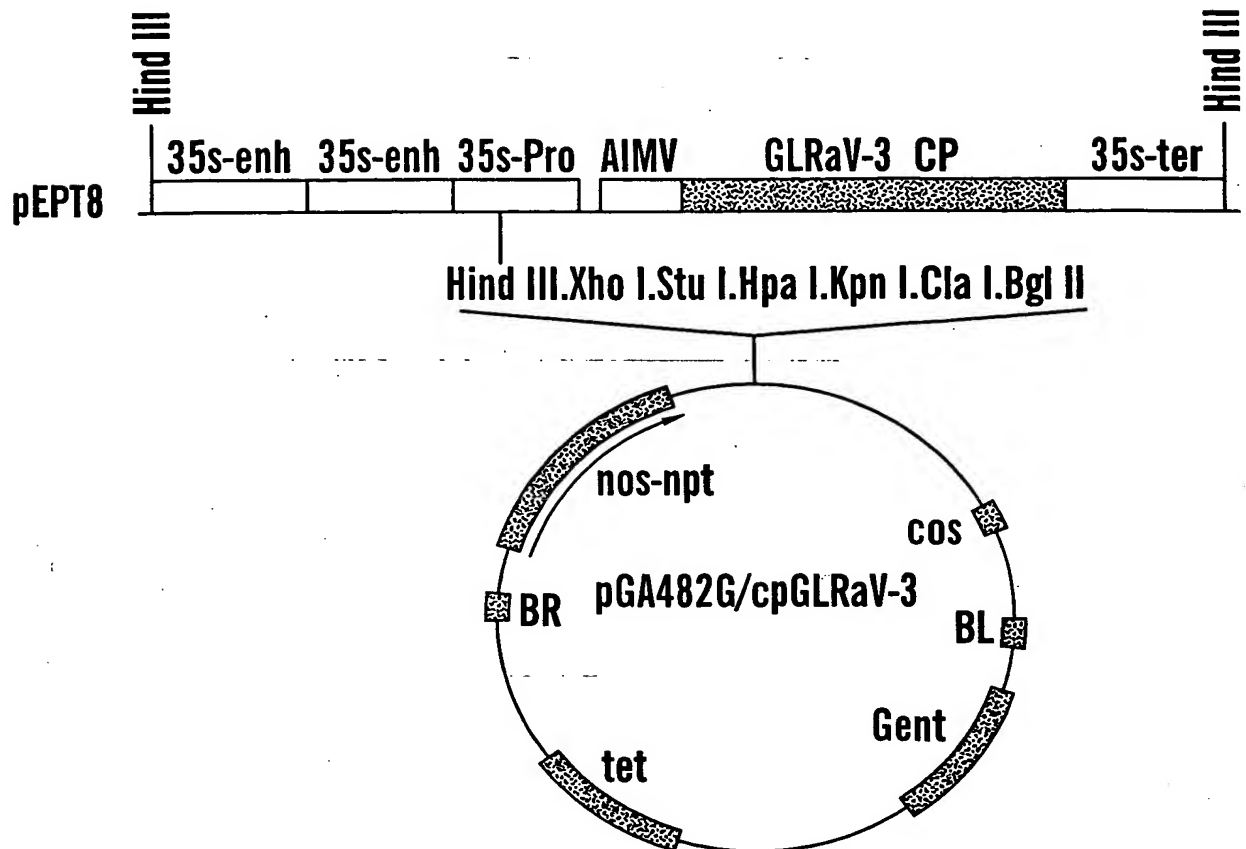


FIG. 32